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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification : C12N 15/11, C12P 21/08 C12Q 1/68, C12N 15/62 C07K 15/28	A2	(11) International Publication Number: WO 94/01548 (43) International Publication Date: 20 January 1994 (20.01.94)
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(54) Title: HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW (57) Abstract <p>This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.</p>		

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HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW

This invention relates to new nucleic acid fragments encoding gene products or portions thereof, which fragments are obtainable from human nucleic acid populations, individual members of such populations being present in widely varying amounts.

5 Situations are increasingly arising in which it is necessary to study complex nucleic acid or polynucleotide populations. For example, it is now widely appreciated that an invaluable resource could be created if the entire sequence of the genomes of organisms such as man were determined and the information available. The magnitude of such a task should not, however, be underestimated. Thus, the human genome may
10 contain as many as 100,000 genes [a very substantial proportion of which may be expressed in the human brain (Sutcliffe, Ann. Rev. Neurosci. 11:157 (1988))]. Only a very small percentage of the stock of human genes has presently been explored, and this largely in a piecemeal and usually specifically targeted fashion.

15 There has been much public debate about the best means of approaching human genome sequencing. Brenner has argued (CIBA Foundation Symposium 149:6 (1990)) that efforts should be concentrated on cDNAs produced from reverse transcribed mRNAs rather than on genomic DNA. This is
20 primarily because most useful genetic information resides in the fraction of the genome which corresponds to mRNA, and this fraction is a very small part of the total (5% or less). Moreover, techniques for generating cDNAs are also well known. On the other hand, even supposing near perfect recovery of cDNAs corresponding to all expressed
25 mRNAs, some potentially useful information will be lost by the cDNA approach, including sequences responsible for control and regulation of genes. Nonetheless, the cDNA approach at least substantially reduces the inherent inefficiencies resulting from analysis of repeated sequences or non-coding sequences in an approach which depends upon
30 genomic DNA sequencing.

Recently, the results of a rapid method for identifying and characterising new cDNAs has been reported (Adams, M.D. et al., Science
35 252, 1991, pp 1651-1656). Essentially, a semi-automated sequence reader was used to produce a single read of sequence from one end of each of a number of cDNAs picked at random. It was shown, by comparing the nucleic acid sequences of the cDNAs (or the protein sequences produced by translating the nucleic acid sequence of the cDNAs) to each

other and to known sequences in public databases, that each of the cDNAs picked at random, could be unambiguously classified. The cDNAs could be classified as being either entirely new or as corresponding, to a greater or lesser extent, to a previously known sequence. cDNAs identified in this way were further characterised and found to be useful in a variety of standard applications, including physical mapping. Unfortunately, such a process is insufficient. The longer the process is pursued with any given population of cDNAs the less efficient it becomes and the lower the rate of identification of new clones. In essence, as the number of cDNAs which have already been picked rises, the probability of picking a particular cDNA more than once increases. This difficulty is exacerbated by the wide range of abundancies at which different cDNAs can occur, which abundancies can vary by several orders of magnitude. Thus, whereas some sequences are exceedingly rare, a single cDNA type may comprise as much as 10% of the population of cDNAs produced from a particular tissue (Lewin, B. Gene Expression, Vol. 2: Eukaryotic Chromosomes, 2nd ed., pp. 708-719. New York: Wiley, 1980). The need to avoid missing rarer species in any given population presents a considerable problem.

Various approaches (so-called "normalisation" techniques) have been tried in addressing the problem of increasing the efficiency of examination of a mixed nucleotide population, for example, such a population as is to be examined in human genome sequencing.

Thus, a standard PCR protocol can be used to amplify selectively cDNAs which are present at extremely low levels, if there is information about the sequence of those cDNAs. If not, a primer specific to the desired cDNA cannot be constructed and the desired cDNA cannot be selectively amplified. The standard PCR method is therefore inadequate if it is desired to characterise a number of unknown genes.

A second approach involves hybridization of cDNA to genomic DNA. At saturation, the cDNAs recovered from genomic/cDNA hybrids will be present in the same abundance as the genes encoding them. This will provide a much more homogenous population than the original cDNA library, but does not entirely solve the problem. In order to reach saturation in respect of the very rare sequences, it will be necessary to use huge quantities of cDNA, which need to be allowed to anneal to large amounts of genomic DNA over a considerable periods of time. Furthermore, cDNAs which are homologous to genes which are present in multiple copies in the genome will be over-represented.

A third approach exploits the second order reassociation kinetics of cDNA annealing to itself. After a long period of annealing, the cDNAs which remain single stranded will have nearly the same abundance, and can be recovered by standard PCR (see Patanjali, S.R. et al., PNAS USA 88, 1991, pp. 1943-1947; Ko, M.S.H., NAR 19, no.18, 1991, pp 5705-5711). The methods disclosed in these two publications, however, suffer from notable disadvantages. They are entirely dependent on the stringent physical separation of single stranded and double stranded DNA, require an elevated number of manual manipulations in each reaction, and necessitate protracted hybridisation times (up to 288 hours in the method of Patanjali et al.)

Yet a further approach in "normalising" a nucleotide population is described in co-pending British Patent Application No 91 15407.0, filed 17th July, 1991 by MRC, and involves a PCR process in which a mixture comprising a heterogenous DNA population and appropriate oligonucleotide primers is first formed and the DNA denatured, but before effecting a conventional PCR protocol the conditions are altered to allow the denatured strands of the more common DNA species to reanneal together, whilst avoiding annealing of primers to the DNA strands. By this means, rarer species can subsequently be amplified in preference to the more common species.

This PCR normalisation method in general comprises the steps of:

- (a) preparing a mixture comprising a heterogenous DNA population and oligonucleotide primers suitable for use in a PCR process, in which the DNA is denatured;
 - (b) altering the conditions to allow the denatured strands of the more common DNA species to reanneal, while preventing the annealing to the primers to the DNA strands;
 - (c) further altering the conditions of the mixture in order to allow the primers to anneal to the remaining single-stranded DNA comprising the rarer DNA species; and
 - (d) carrying out an extension synthesis in the mixture produced in step (c).
- Advantageously, the method consists of a cyclic application of the above four steps.

It will be appreciated that the conditions may be altered by the alteration of the temperature of the reaction mixture. However, any conditions which affect the hybridisation of complementary DNA strands to one another may be varied to achieve the required result.

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Because the reannealing efficiency of any given DNA species will depend on the product of its concentration and time, the more abundant the sequence the greater the extent to which it will reanneal in any given time period. Once a DNA species has reached a certain threshold concentration it will no longer be amplified exponentially, as a significant amount will have annealed to the double stranded form before the priming step. Thus, as each individual DNA species is amplified by the process to its threshold concentration, the rate of amplification of that species will start to tail off. Eventually, therefore, all DNA species will be present at the same concentration.

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The length of the reannealing step will determine how much DNA is present at the threshold concentration. Preferably, therefore, the duration of the reannealing step will be determined empirically for each DNA population.

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In the PCR normalisation process in general, the DNA primers may be adapted to prime selectively a sample of the total DNA population. By using primers which will only prime a sample of the population, only that sample will be amplified and normalised. The total quantity of DNA generated will thereby be reduced, which means that the cycling times can be kept low. This ensures that the method is applicable to complex DNA populations such as cDNA populations. In addition, a first primer can be used which is adapted selectively to prime a sample of the total cDNA population, and a second primer which is a general primer. Advantageously, the general primer is oligo dT (each primed cDNA will then be replicated in its entirety, as the oligo dT primer will anneal to the poly-A tail at the end of the cDNA).

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In co-pending British Patent Application No 92 14873.3, filed by MRC 13th July, 1992, a new process is described which allows the study and identification of the individual members of a mixed or heterogeneous population of nucleotide sequences perhaps of varying abundance. In preferred embodiments of the said process, the starting nucleic acid population is treated by:

- (a) subjecting the nucleic acid to the action of a reagent,

preferably an endonuclease which has its cleavage and recognition sites separated, which reagent cleaves the nucleic acid so as to produce double stranded cleavage products the individual strands of which overlap at cleaved ends to leave a single strand extending to a known extent;

(b) ligating the cleavage products from (a) with a population of adaptor molecules to generate adapted cleavage products, each of which adaptor molecules has a cleavage product end recognition sequence and the population thereof encompassing a range of adaptor molecules having recognition sequences complementary to a predetermined subset of the sequences of the cleavage-generated extending single strands; and

(c) selecting and separating only those adapted cleavage products resulting from (b) which carry an adaptor of predetermined recognition sequence.

A preferred endonuclease for use in step (a) of the above process is Fok I.

An important feature of this process is the use of adaptor molecules. The adaptors used must have "overhanging" fragment recognition sequences which reflect or are complementary to the extending cleavage-derived sequences which the adaptors are designed to react with. It is also preferred that the adaptors used should end with a 5' hydroxyl group. The avoidance of a 5' phosphate group removes the risk of inappropriate ligation involving the adaptors.

Adaptor molecules may also contain a portion permitting specific sequence selection and separation (as in step (c) of the process) when a sequence is attached to the adaptor. For example, an adaptor can carry biotin, thereby permitting advantage to be taken of the biotin/avidin

reaction in selecting and separating desired adapted molecules. Additionally, adaptors preferably comprise a known and selected sequence such that specifically isolated adapted molecules can be amplified by known techniques (such as PCR) using a primer complementary to the core sequence.

Preferably the adaptors are short double-stranded oligonucleotides which can be joined to the ends of cleavage products. They will have been chemically synthesised so that their sequence can be predetermined

and so that large concentrations can be easily produced. They may also be chemically modified in a way which allows them to be easily purified during the process. As mentioned above, ideally their 5' ends will be unphosphorylated so that once joined to fragments the adaptor end of the latter will no longer be able to participate in further ligation reactions.

It is preferred that the adaptor cleavage product end recognition sequences are on the 5' end of the longest oligonucleotide strand making up the preferred adaptor molecules, are at least 3 nucleotides in length and with totally random bases at the single-stranded position(s) two nucleotides in from the 5' end. This then allows selection to be performed both during the joining reaction and during subsequent priming reactions. Then, because the final degree of selection is a result of the product of the degrees of selection achieved at these two stages, maximum selection can be achieved per adaptor/primer available.

Adaptor strand extensions on the 5' end of the longest oligonucleotide also facilitate the use of modified oligonucleotides for separation purposes. Preferably, the short oligonucleotide will be modified at its 5' end. This has the double benefit of requiring just one modified oligonucleotide for all possible single-stranded extensions that are used, and also placing the modification at a position where it cannot interfere with ligation or subsequent priming reactions.

Although only one type of adaptor is required per ligation reaction, it is preferred that adaptors covering all possible reactions in a chosen subset of sequences be present, because then the opportunity for fragments in the chosen subset to ligate to each other is minimised. It is also preferred that the chosen specific adaptor, carrying a predetermined recognition sequence, should not only be different from the other adaptors in its single-stranded extension, but also different in the rest of its sequence since this allows orientation to be introduced which is useful in subsequent steps. It is therefore also preferred that this adaptor has a modified oligonucleotide to facilitate its separation with the cleaving products to which it joins.

The above "adapting" process can be used to generate categories or subsets of sequences by making some of the adaptors specific in some way, and selecting and separating as in step (c). In this way subsets of sequences can be provided depending upon the specific adaptor

chosen, e.g. for use in subsequent nucleotide sequencing. This facilitates, for example, the identification of a large population of sequences by permitting a rational approach to splitting such populations into subsets, each of which subsets can be examined in turn.

In the light of these developments, the present invention now provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-

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(a) a sequence selected from SEQ ID Nos 1 to 1193;

(b) an allelic variation of a sequence as defined in (a); or

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(c) a sequence complementary to (a) or (b).

In another aspect, the invention provides a nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof. Preferred sequences exhibit no more than 90% homology to a human sequence known per se.

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In a further aspect, the invention provides a nucleic acid fragment comprising a portion of a sequence as defined above of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridise to said sequence. Preferably, such portions are at least 15 bases in length. It will be appreciated that minor mismatches in the aforesaid "complementarity" are not excluded provided hybridisation can still occur. In general, hybridisation conditions are within the choice of the skilled person, but reference can be made, for example, to the following: Melting temperature of hybrids - Bolton, E. T. and McCarthy, B. J. Proc. Natl. Acad. Sci, 48 p1390 (1962). Effect of formamide on lowering melting temperature - Casey, J. and Davidson, N., Nucleic Acids Res. 4, p1539 (1977). Effect of imperfect homology - Bonner, T. I. et al., J. Mol. Biol. 81, p123 (1973). General - Meinkoth, J. and Wahl, G. Anal. Biochem. 138, p267 (1984). Oligo hybridization and washing - Lathe, R. J. Mol. Biol. 183, P1 (1985).

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The present invention also envisages DNA constructs comprising fragments or sequences as referred to above with a control or regulatory sequence.

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The invention includes such DNA constructs using a gene system known in the art ligated to a sequence or fragment of the invention so as to enable, upon expression, the provision of a fusion polypeptide. Preferably, an endopeptidase recognition site is provided such that when the sequence or fragment is expressed it is expressed in frame with a known protein with the boundary being a cleavage site for an endopeptidase with a rare cutting site. The known protein can then be affinity purified, and the peptide corresponding to the fragment or sequence in accordance with the invention may be released by the endopeptidase. Alternatively, the whole protein can be used to raise antibodies which can then be screened for those directed at polypeptide corresponding to the fragment or sequence of the invention.

Since the present fragments and sequences can be used to produce, inter alia, corresponding genes, whether by isolating them, by synthesis or otherwise, such use and the resulting DNA fragments comprising genes are further aspects of the invention.

Yet another aspect of the invention is an expression vector comprising a fragment, sequence, gene-comprising DNA fragment, or DNA construct, as above, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory sequence.

Other aspects of the invention are host cells incorporating a sequence, or fragment, or gene-comprising DNA fragment, or DNA construct, as above, as a heterologous part of the expressible genetic information of the cell. The production of such modified host cells can be achieved using methods known in the art. Such modified host cells can be used to express corresponding proteins, and these materials lend themselves in turn to the preparation of corresponding monoclonal or polyclonal antibodies using standard techniques.

Also included in this invention are such antibodies. Reference can be made, inter alia, to the following literature: Monoclonal antibodies, Cambell, A. M. Laboratory Techniques in Biochemistry, and Molecular Biology Ed. Burdon, R. H. and van Knippenberg, P. H. vol 13. Elsevier Amsterdam 1984. Goding, J. W., Monoclonal antibodies: Principles and Practice, 2nd Edition, academic Press, London 1986. Kipps, T. J. and Herzenberg, L. A., Handbook of Experimental Immunology : Applications of immunological methods in biomedical sciences, 4th edition Ed. Weir,

D. M. et al., p108 Blackwell scientific Publications, Oxford. Harlow, E and Lane, D. Antibodies, A Laboratory Manual, Cold spring harbor Laboratory, Cold Spring, New York.

5 Expression in an appropriate higher eucaryotic host may be important to ensure correct protein folding and also activity. Expression to avoid copurification of toxic products can sometimes be better performed in organisms approved for human consumption, eg prokaryotic *Bacillus subtilis*, eukaryotic yeast, mammalian cows milk vectors, and other
10 methods known in the art.

The invention also includes novel gene products or portions thereof encoded by a fragment, sequence or gene-comprising DNA fragment of the invention.

15 It will be appreciated that the sequences of the present invention collectively have utility based, inter alia, upon their common origin, and hence they can effectively be considered together rather than as separate entities. It is convenient to represent them as separate
20 sequences, because this is how they were produced and serves as "punctuation" between the different functional entities which each sequence represents. However, the sequences could just as easily have been presented as a continuous sequence derived by placing them end to end in the order in which they were produced, with a separate
25 indication of where the beginnings and ends of the component sequences are.

In contrast to investigations hitherto, where gene fragments (sequence fragments) could only be identified through some known characteristic
30 [for example: their homology to a fragment which largely encodes amino acids identified by sequencing a previously isolated peptide or is the antisense of that coding sequence; or them having at least partial homology to previously characterised nucleic acids; or them having ability to encode expressed proteins which could later be detected by
35 functional assays of the cells expressing those proteins or by using antibodies which had been previously raised against the proteins to detect their expression, Sambrook J., et al., Molecular Cloning CSH Press 1989], the sequences and fragments described by the present invention are entirely underivable and unpredictable from the prior
40 art, but are nonetheless clearly of great value for various purposes.

Thus, such sequences, by comparing them to sequence databases, can be

used as a means for determining the existence of new members of existing gene families, new human genes when previously only non-human genes were known and new genes when previously no genes were known (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1980)). In all cases, this allows the isolation of the corresponding genes and their products, and hence enables the manufacture of molecules of potential biological interest by recombinant means. Screening libraries of known materials or hitherto unexplored source materials for biological efficacy is now an important industrial activity in the search for new therapies and therapeutics. When new sequences have already been found to have counterparts in gene families or in non-human genes then knowledge about biological efficacy may already be apparent. For example, new receptors or receptor agonists/antagonists may exhibit differences to known instances of these molecules, and such differences could make them more suitable as therapeutics by, for example, exhibiting binding characteristics which are more in keeping with avoidance of toxicity. Reference can be made, for example, to polymorphic dopamine receptors and the implications for mental health (Iversen, L. Nature 358, p109 (1992), and Van Tol, H. M. M. et al., Nature 358, p149-152 (1992)). Where absolutely required, realisation of full length cDNAs for expression can be achieved by using the sequences to screen (by hybridisation) suitable cDNA libraries containing full length clones (D'Alession, J. M., et al., Focus (Gibco B.R.L) 9 p1 (1987)). Alternatively, the sequences can be used to design primers suitable for obtaining the missing sequences by PCR or other amplification methods (Frohman, M. A., Dush, M. K. and Martin, G. R., Proc. Natl. Acad. Sci. 85 p8998-9002 (1988)).

Appropriate use of the sequence fragments in antisense or triple helix (Griffin et al., Science 245 p967-971 (1989)) applications will be useful for identifying manipulable targets related to disease. For example, viruses have been inhibited by antisense RNA to their mRNAs (Chang, L-J., and Stoltzfuz, C. M. J. Virol. p921-974 (1987)). A similar effect could be achieved by targetting the expression of cellular proteins which are essential for growth or maintenance of the virus.

Partial or full length cDNAs have great utility once expressed. The manner of expression can be selected by one skilled in the art to suit the intended application. Expression of full length cDNAs is typically required for biological activity. Prokaryotic, and lower or higher eucaryotic hosts may be selected as the host for expression and higher

eucaryotes may be preferred to ensure correct modifications, for example, glycosylation in vivo, when this proves to be important. Expression can be ensured by situating the cDNA appropriately to signals for expression (Amann, E. and Brosius, J. *Gene* 40 p183 1985), Shimuzu, Y et al., *Gene* 65, p141 (1988), Straus, D. and Gilbert, W. *Proc. Natl. Acad. Sci.* 82, p2014 (1985)). Such signals may include a promoter for transcription, which may itself be regulatable.

The proteins thus-expressed can be screened for activities of therapeutic or commercial value. It may be that the proteins have to be first isolated for this purpose or can be assayed in situ. It may be desirable that some means of stabilising the expressed protein is employed. This can be achieved, for example, (and as indicated earlier) by expressing in frame as part of a fusion polypeptide (Smith, D. B., et al., *Proc. Natl. Acad. Sci.* 83 p8073 (1986)).

Useful antibodies can be raised against the expressed proteins. It is commonly not an absolute requirement that full length proteins are produced, although this may influence the quality of the antibodies produced. Peptides as short as 8 or 9 amino-acids in length can be used as antigens (Germain R., N. *Nature* 353 pp605-607 (1991), Rudensky, A., Y., et al., *Nature* 353 p622-627 (1991)). Immunogenic peptides could simply be synthesised using the amino-acid sequence translated from a sequence or fragment of this invention. It is desirable, although not absolutely required, that some means of producing purified antibodies is adopted. When fusion polypeptides are used to raise antibodies, an affinity matrix specific for the generic part of the protein allows the fusion polypeptide to be immobilised (Smith, D. B., et al., *Proc. Natl. Acad. Sci.* 83 p8073 (1986)). The immobilised polypeptide can then be used to affinity purify the antibodies. Antibodies to both the generic part of the fusion polypeptide and the part of interest are produced. When these need to be discriminated between, a different affinity column can be used to remove only those antibodies specific for the generic part of the polypeptide. Alternatively, and as mentioned earlier, it can be arranged that the boundary between the two separate protein components of the fusion polypeptide has the recognition sequence for an endopeptidase with a rare cutting site. The peptide of interest can then be released from the affinity purified polypeptide by the action of the endopeptidase (Nagai, K., and Thogersen, H., *C. Methods Enzymol.* 153 p461-481 (1987)). Another alternative is raise monoclonal antibodies against the purified protein.

The antibodies can be used for localising in situ, or quantifying in samples through, for example, ELISA or RIA assays, peptides against which they were raised. These uses are particularly beneficial when the results of the assays can be correlated to a disease condition, eg cancer. For example tumour markers may be found and used to target therapeutic agents. The antibodies can also be used to detect or monitor markers of undifferentiated growth, infection, cardiovascular or immune disease or a therapeutic response. When the antibodies recognise cell surface proteins they can be used in isolation or in combination to isolate particular populations of cells. These in turn can be used to isolate yet more cDNAs which will be enriched for yet more of such surface markers for the population, which, if similarly screened, will permit yet further subdivision of the population. Ultimately, panels of antibodies which can describe particular disease states will accrue. Such antibodies could be tailored for forensic applications as well as diagnostic purposes and disease monitoring.

The sequences or fragments can also be used for genetic analysis and mapping, for example, to diagnose the likelihood that a given individual is predisposed towards a given genetic disease. In the event of a sequence co-locating, genetically, with a disease gene, it can be used for the derivation of new disease therapies bases upon precise genetic knowledge. Such therapies can include, for example, the techniques of so-called "gene therapy" (Dusty Miller, A. Nature 357 p455-460 (1992)).

Antibodies can be produced against the protein of a genetic disease with sufficient discriminating power to discriminate between diseased and non-diseased states (Caskey, T. Genome Sequencing Conference, Hilton Head, S. Carolina (1991)). This would be useful for reducing the dependence of such tests on nucleic acid-based screens. Such antibodies also have the advantage of allowing detection of faulty expression of the protein, for example levels of expression which may be important for development of the disease in slow onset conditions.

Also very important is that not all cDNAs are likely to be found by conventional means, whereas the present sequences are, in one sense, "comprehensive". The use of the class of cDNAs which corresponds of necessity to truncated clones increases the chances that part of a cDNA will be cloned free of any sequences that could otherwise compromise it from being cloned. Sequence obtained can then be used to generate PCR primers from which the remainder can be obtained without having to

clone.

This invention will now be further described and illustrated by means of the following Examples.

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All oligonucleotides used in these Examples were synthesised Trityl on using an ABI 380B DNA Synthesizer according to the manufacturers instructions. Purification was by reverse phase HPLC (see, for example, Becker, C., R., et al., J. Chromatography 326, p293-299 (1985)).

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Example 1

Human brain and adrenal tissues were obtained from a mixture of 12 to 15 week menstrual age fetuses and then snap frozen in liquid nitrogen before storing in bijoux bottles in a -80°C freezer. The two types of tissue were used separately, directly from the freezer, to prepare cDNA from which restriction fragments were generated for sorting into subsets. 1g portions of each of the separate tissues were homogenised, using an Ultra-Turrax T25 Disperser (Janke and Kunkel, IKA-Labortechnik), on ice in the presence of 4M guanidinium isothiocyanate to solubilise macromolecules. RNA was isolated from each homogenate by using centrifugation to sediment it through caesium trifluoroacetate. This was performed using the Pharmacia kit according to the manufacturer's instructions, except that centrifugation was performed for 36 hours and the RNA obtained was finally desalted and concentrated by performing two ethanol precipitations in succession with two 70% ethanol washes after each precipitation. In each case, polyA⁺ (mRNA) was isolated from 200 to 400 µg of the total RNA by binding it to magnetic oligo-dT coated beads (Dynal). Solution containing unbound material was removed from the beads, which were washed, and then mRNA eluted directly for use. mRNA isolation was performed in accordance with the manufacturer's instructions. Yields of RNA from the beads were between 1 and 3% of the total RNA. 2 to 4 µg of the eluted RNA were used for cDNA synthesis. cDNA synthesis was performed according to the method of Gubler, U and Hoffman, (B. J. Gene 25 p263 (1983) using a Pharmacia kit according to the manufacturer's instructions. OligodT was used to prime the first strand cDNA synthesis reaction. The cDNA was purified by extracting twice with phenol/chloroform and then low molecular weight solutes including nucleic acids below ca. 300 bases were removed by passing the cDNA reaction mixture through a Pharmacia S400 spun column used according to the manufacturer's

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instructions. Running buffer for the column comprised 10 mM TrisHCl, 1 mM EDTA, 50 mM NaCl @ pH 7.5.

5 The column eluate was adjusted to 10 mM Mg^{2+} and then the purified cDNA was restricted by the action of 1 unit per 10 μ l of the endonuclease Fok I at 37°C for 1 hour, so that it would be able to accept adaptors to enable fragment sorting.

10 The cDNA fragments were purified by two successive phenol/chloroform extractions followed by passing them through S400 spun columns as described above.

15 The adaptors used were oligonucleotides 5' $N_4N_4N_4N_4$ TCCTTCTCCTGCGACAGACA (SEQ ID: 1194) with the complementary strand 5' TGTCTGTGCGAGGAGAAGGA (SEQ ID: 1195) and 5' AAN_4N_4 TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1196) or 5' TTN_4N_4 TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1197) each with the complementary 5' biotinylated strand GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198). These were added to 25% of the eluted material by incubating together 200 pmoles of the mixture of double-stranded adaptors in the elution buffer to which had been added $MgCl_2$ to 10mM, ATP to 10mM and 0.025 units/ μ l of T4 DNA ligase. The oligonucleotide 5' biotinylated GTTCTCGGAGCACTGTCCGAGA, (SEQ ID: 1198) and whichever of the complementary oligonucleotides with which it was used, each comprised 1/32 of the molar proportion total adaptors. The final reaction volume was 90 μ l which was heated to 65°C for 3 minutes and then cooled to room temperature before the ligase was added. Ligation was performed for 16 hours at 12°C.

25 Two successive phenol/chloroform extractions were performed to remove the ligase. The final aqueous phase was passed through an S400 spun column (Pharmacia) as described above except that the column was used with 10 mM Tris pH 8.3/50 mM NaCl.

35 The column eluate was adjusted to 25mM Mg^{2+} , 0.5mM dNTPs in a final volume of 200 μ l. The mixture was placed in a thermocycler (Techne MW2) and heated to 78°C for 5 minutes. At this point 10 units of cloned Taq DNA polymerase (AmpliTaq, Perkin Elmer) were added. This was followed by an incubation at 72°C for 10 minutes to fill in the unligated strand of the adaptor. After the second incubation 200 μ l of streptavidin coated magnetic beads (Dynal) prepared according to the manufacturers instructions were added to bind cDNA ligated to that of the oligonucleotides which was complementary to the 5'

GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198) biotinylated adaptor. Bead binding was allowed to proceed at 28°C for 30 minutes with mixing every 10 minutes.

5 Un-biotinylated cDNAs were washed from the beads with 400 µl each of 2M NaCl twice, fresh 0.15 mM NaOH four times at 28°C for 5 minutes each, water twice and finally a buffer comprising 20 mM Tris pH 8.3, 50 mM NaCl, and 25mM Mg²⁺. The beads were then resuspended in 240 µl of the final buffer including additionally 0.5 mM dNTPs and divided into 4x60
10 µl.

Four of the 60 µl aliquots, two from each tissue, were processed further specifically to prime and copy a subset of the immobilised, adapted fragments. 2 pmoles of the primer 5' CTGTCTGTCGCAGGAGAAGGAA
15 (SEQ ID: 1201) were added to each of two aliquots, one from each tissue. 2 pmoles of the primer 5' CTGTCTGTCGCAGGAGAAGGAG (SEQ ID: 1202) were added to each of the other two aliquots. 2.5 units of Taq DNA polymerase were added to each reaction and 16 cycles of alternate denaturation at 95°C for 30 seconds, annealing at 63°C for 2 minutes
20 and polymerisation at 72°C for 3 minutes was performed to accumulate the selected single-strands in solution.

On completion of the DNA synthesis reactions a further 30 µl of resuspended beads were added to each reaction to remove the
25 biotinylated fragments. The reaction was incubated at 28°C for 30 minutes mixing every 10 minutes to ensure that the biotinylated strands were bead bound. Each aqueous phase containing the newly synthesised strands was then removed and extracted with phenol/chloroform twice to remove the enzyme before being further purified by passing through an
30 S400 spun column equilibrated with 10 mM Tris pH 8.3/50 mM NaCl as described above.

Rounds of PCR amplification of subsets of the selected fragments were performed by using the original primer in each case, together with one
35 of the primers 5' GTTCTCGGAGCACTGTCCGAGAG (SEQ ID: 1199) or 5' GTTCTCGGAGCACTGTCCGAGAC (SEQ ID: 1200). This simultaneously rendered the fragments double-stranded and increased the amounts of available material. It was not known how many cycles of amplification would be required at this stage, since each primer pair would be expected to
40 behave differently. It was therefore necessary directly to determine a suitable number empirically by using standard agarose gel electrophoresis to examine the reaction products after a given number

of cycles. In some cases, to avoid the accumulation of non-specific products, it was necessary to perform an initial 5 cycles of amplification with both of the primers present at 2 pmoles each. All reactions were performed using 8 μ l or 12.5 % whichever was the larger but not exceeding 12 μ l of the column effluent above. Reaction conditions were adjusted to 20 mM Tris pH 8.3, 50 mM NaCl, 25mM Mg^{2+} , 0.5mM dNTPs and 2.5 units of Taq DNA polymerase in a final volume of 40 μ l. Apart from when an initial amplification with 2 pmoles of each primer was performed, 20 pmoles of each primer were used. Cycles of amplification were performed at 95°C for 30 seconds, 65°C for 1 minute and 72°C for 3 minutes.

For the purposes of cloning, selected cDNA was amplified as described immediately above, except that the reaction was not monitored. Instead, the number of cycles which had previously been shown to just give rise to all observable products plus another 4 cycles were performed. In addition, an extra 72°C for 10 minutes incubation was performed after the last cycle.

The products of the reaction were then prepared for directional cloning. Water was added to adjust the final reaction volume to 60 μ l. Enzyme was removed by two successive phenol/chloroform extractions. The final aqueous mixture was passed through an S400 column as described above, except that it had been equilibrated with 10 mM Tris HCl pH 7.5, 50mM NaCl.

For directional cloning, advantage was taken of the different known sequences introduced at each end of the selected cDNAs by the adaptors in a modification of the method of Aslandis, C. and de Jong, P. J. (Nucl. Acids Res. 18, p6156 (1990)). Different cohesive ends were produced on each end by using the exonuclease activity of T4 DNA polymerase to resect from the 3' end, to the first T in each case. To 75 μ l or 75 % of the column eluate, whichever was least, were added 9.5 μ l of 100mM TrisHCl pH7.4, 100 mM $MgCl_2$, and 9.5 μ l of 0.5 mM dTTP. 16 units of T4 DNA polymerase were added and the reaction incubated in a water bath at 37°C for 30 minutes. The enzyme was removed by extracting with phenol/chloroform, twice successively. The salt of the final aqueous phase was adjusted by passing it through an S300 column (Pharmacia) equilibrated with 10 mM TrisHCl pH 7.4, 1 mM EDTA as described above.

The E.coli plasmid cloning vector pBluescript KS+ (Alting-Meese, M. A.

and Short J. M., Nucl. Acids Res. 17 p9494) was prepared for accepting the resected cDNA by restriction cleavage at the BamHI and HindIII sites and then adaptor the resultant cohesive ends using the specific adaptors produced by the oligonucleotide 5' AGCTCGGCTCGAGTCTG (SEQ ID: 1203) with its partially complementary oligonucleotide 5' GCGACAGACAGCAGACTCGAGCCG (SEQ ID: 1204) and the oligonucleotide 5' GATCCGGCTCGAGT (SEQ ID: 1205) with its partially complementary oligonucleotide 5' CCGAGAACAACCTCGAGCCG (SEQ ID: 1206). Preparation of the vector and adaptor were performed according to standard procedures. Insertion of the cDNA was performed between the BamHI and HindIII restriction sites. Recombinant vectors were transformed into the host XL1-Blue (Bullock, W. O. et al Biotechniques 5 p376-378 (1987)) by the method of Hannahan, D. J. (Mol. Biol. 166 p577-580 (1983)). Suitable standard controls for the ligations and transformations were also included.

Post transformation procedures were as described in "Molecular Cloning", 2nd Edition (Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). Colonies were produced by plating onto X-gal/IPTG L-agar plates containing 50µg/ml ampicillin and 10µg/ml tetracyclin. Clear colonies were picked, each into a separate well of a microtitre plate, containing 100µl of L-broth and 50µg/ml ampicillin. Growth was allowed to occur for 16 hours at 37°C. 100µl of 50% or 30% glycerol was added to plates which were archived at -20°C or -80°C, respectively.

Bacteria corresponding to those archived were used for preparing templates for sequencing by the dideoxy method (Sanger, F. Milklen, S. and Coulson, A. R. Proc. Natl. Acad. Sci. 74 p5463-5467 (1977)). Bacteria for this purpose were either grown on L-agar plates containing 50µg/ml of ampicillin, prepared at the same time as they had been grown in liquid culture, or after plating out from the archive. Alternatively, fresh liquid cultures were inoculated from the archive. In all cases, cDNA inserts were amplified for sequencing by PCR (Saiki, R. K. et al Science 239 p487-491 (1988)). PCR was either performed using bacteria directly added to the reaction, by a toothpick, or PCR was performed using 1/50th of the plasmid isolated by preparative methods (Holmes, D. S. and Quigley, M. Anal. Biochem. 114 p193 (1981)) from the bacteria in the liquid cultures or from the plates.

20 pmoles of each of the PCR primers 5' biotinylated GTAAACGACGGCCAGT

(SEQ ID: 1207) and 5' CGAGGTCGACGGTATCG (SEQ ID: 1208) were used in 40µl reactions containing 2.5mM Mg²⁺, 50 mM KCl, Tris-HCl pH 8.3 and 0.25 units of Amplitaq (Cetus). Reactions were performed at 95°C, for 1 minute, followed by 35 cycles at 95°C for 30 seconds, 60°C for 30 seconds and 72°C for 40 seconds. After the cycles, a final incubation at 72°C for 5 minutes was performed.

After PCR, standard agarose gel electrophoresis was used to determine which reactions had been successful. The biotinylated strands of successful reactions were then recovered for single-stranded sequencing by binding them to streptavidin coated beads (Dynal) and then washing, all according to the manufacturers instructions, except that the washing steps were either performed manually or performed automatically in the 96 well microtitre plate format using a Biomek robotic workstation attached to a side-arm loader (Beckman).

Dideoxy chain termination sequencing reactions were performed using the immobilised, biotinylated strands as templates and 2 pmoles of the oligonucleotide 5' CGAGGTCGACGGTATCG (SEQ ID: 1209) as primer. Reactions were performed using fluorescently-labelled terminators (Du Pont) or a fluoroscein-labelled primer (Pharmacia) according to the manufacturers instructions. Reactions were analysed using automated DNA sequencers. A Genesis 2000 was used for the "Du Pont" reactions and an A.L.F. for the "Pharmacia" reactions. Bases were assigned for the Genesis 2000 reads using the manufacturers Base Caller software. Files of called bases were then transferred to a SUN Network from an Apple Macintosh computer which had been used for base calling. Raw data from the A.L.F. reads was directly transferred to a SUN network where bases were called using the public domain "trace editor software" (TED). In both cases, files of called bases were entered into a Sybase™ database. Entering data entailed automatically removing vector and adaptor or linker sequences, but not editing ambiguous bases. After removal of the unwanted bases, files were automatically compared to other sequences in the cDNA database and the latest versions of the publically available databases, GENBANK and SWISSPROT. Searches were performed with the "basic local alignment search tool" (BLAST) (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1990)).

Sequences SEQ ID Nos 1 to 610, given hereinafter, were obtained by the above procedure.

Example 2

A second method of preparing cDNA libraries for obtaining gene fragments of the invention took advantage of the PCR normalisation process described above. Standard procedures were used to prepare mRNA from RNA that had been isolated by standard caesium chloride bouyant density gradient methods from a full term human placenta. The oligonucleotide LNotdt, sequence 5' TACGTTGACAAGCTTGAATTCGGGCCGC(T)₂₆, (SEQ ID: 1210) was used at 1 μ M with AMV reverse transcriptase, to prime first strand cDNA synthesis under standard conditions from 0.5 μ g of the placental mRNA. Temperatures above 65°C were used to inactivate the reverse transcriptase and then the volume of the reaction made up to 100 μ l with water.

PCRs were then performed in reactions containing 1 μ l of the diluted cDNA, 10 mM Tris-HCl pH 8.3, 40 mM KCl, 1.5 mM MgCl₂, 0.01% gelatin, 200 μ M dNTPs, 10 uCi a³²P dCTP, 1 μ M each of the primers 11AD1, sequence 5' GCC(TA)(GC)CGCCGA (SEQ ID: 1211), and LNotdT and Taq DNA polymerase. An initial denaturation period of 95°C for 90 seconds was followed either by 35 cycles of standard PCR, comprising 95°C for 30 seconds, 45°C for 30 seconds and 72°C for 30 seconds or alternatively 3 cycles of the standard PCR already described followed by 27 cycles of Cot PCR during which an additional step of 72°C for 16 minutes was placed between all of the 95°C and 45°C steps of the standard PCR. The standard PCR was followed by a single 72°C for 3 minutes step while the Cot PCR was followed by one standard PCR cycle except that the 72°C incubation was performed for 3 minutes.

Products of the PCR reaction were end repaired by adding 5 units of T4 DNA polymerase to the reaction and then incubating at 37°C for 10 minutes. Enzymes were removed by phenol extraction. The cDNA was precipitated by 70% ethanol, dried and then resuspended in NotI buffer. 20 units of NotI were used to digest the cDNA under standard conditions. cDNA was again phenol extracted and ethanol precipitated. 10% of the purified NotI cut DNA were ligated to the vector pBluescript lting-Meese, M. A. and Short J. M. Nucl. Acid Res. 17 p9494 which had been prepared as standard to receive this DNA by restricting with the enzymes NotI and EcoRV. Transformation and processing of clear colonies was performed as described above except that the host E.coli strain DH5a was used in place of XL-1 Blue.

Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced were performed as described in Example 1.

Sequences SEQ ID Nos 611 to 772, given hereinafter, were obtained by the above procedure.

Example 3

5 cDNA libraries corresponding to adult brain cortex (Clontech Laboratories, Inc., Cat No. HL10036) and adult bone marrow (Clontech Laboratories, Inc., Cat No. HL10586) prepared in lambda gt11 phage were transfected into E.coli Y1090 and plated out for colour selection of
10 recombinant plaques ("Molecular Cloning", 2nd Edition Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). 192 lambda Zap clones, corresponding to rhabdomyosarcoma cDNAs and a gift from C. Cooper, ICR, Sutton, were similarly plated except that the host XL-1 Blue was used.

15 Clear plaques from each library were resuspended in 5 μ l of Tris-HCl pH 8, 1 mM EDTA. 2 μ l of the resultant phage suspensions were added directly to PCRs for the purpose of amplifying the cDNA inserts for sequencing. PCR was performed as described in Example 1, except that
20 the oligonucleotides used as primers for the lambda gt11 clones were 5' GGTGGCGACGACTCCTGGAGCCCG (SEQ ID: 1212) and 5' TTGACACCAGACCAACTGGTAATG (SEQ ID: 1213). Whichever of the oligonucleotides was to be used to prime the strand which would serve as the sequencing template was used in biotinylated form.

25 Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced was performed as described in Example 1, except that 2 pmoles of the primers that were unbiotinylated in the PCR were used as sequencing primers.

30 Sequences SEQ ID Nos 773 to 1193, given hereinafter, were obtained by the above procedure.

35 The following are the SEQUENCE LISTINGS which comprise sequences SEQ ID Nos 1 to 1213 referred to hereinbefore. Certain of these sequences are preferred, and are listed as such after the main SEQUENCE LISTINGS.

(1) GENERAL INFORMATION

(i) APPLICANT

(A) NAME: MEDICAL RESEARCH COUNCIL

5 (B) STREET: 20 PARK CRESCENT

(C) CITY: LONDON

(E) COUNTRY: ENGLAND

(F) POSTAL CODE: W1N 4AL

10 (ii) TITLE OF INVENTION: HUMAN GENOME SEQUENCES

(iii) NUMBER OF SEQUENCES: 1213

(iv) COMPUTER READABLE FORM:

15

(A) MEDIUM TYPE: DISKETTE

(B) COMPUTER: IBM PC COMPATIBLE

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: EXTRACT

20

(2) INFORMATION FOR SEQ ID :1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1:

GCCGATTCGT GACCAAGAAG GCTCTGTGCA TTCGGGTTTT CCAGGAGACT 50

35 CAAAAGCTGA AGAAGCGAAG AAGAGCCTTA AAGGCTGCAG CAGCAGCTCA 100

ATAACAAGC AAAGCGGAGG AACCCAGACA GCCCTTGTCC AAAGCCATAC 150

CAATATGATC TATCTTCTAA TGTATCCATG TTGTAATTAT ATATGTGTCT 200

40

GTGTGTGTCG AAATCTCTAG ACATACAGAT ATATATTCAT ATATCATATA 250

22

264

TATATATATA CACA

(2) INFORMATION FOR SEQ ID :2:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :2:

15 AGGAACATGT GTTTATTCAT CCAGCAGTGT TGCTCAGCTC CTACCTCTGT 50
GCCAGGGCAG CATTTTCATA TCCAAGATCA ATTCCCTCTC TCAGCACAGC 100
CTGGGGAGGG GGTCAATTGTT CTCT 124

20

(2) INFORMATION FOR SEQ ID :3:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :3:

ACAGAGCCGA TTCTGCATCC ACTGTGGTCA ACATTTAGGA AGTTTTAAGC 50
35 TAAGATTTGC CAAATTGTAG CCTACTGGAT TCCGGTTCTC TTGACATCTC 100
TTTCTAGTAG CCATGTCTTG CACTTCCCGA GTATAACGA ACTGAGATGC 150
AAATTAAAAA AGGGAGGATT TAGAATAATG AAAAGAGAAA AGTCAAGAAA 200
40 GCACAATCAC TAGTGTAGAG ATAACAGAAT TTCTGAATTC CCTGAAAGCA 250

23

ATCTATATAA ATGCATGTGA AATAATACAC CAGCATCTGT GGCCCATACG 300
TCACATATTA GGAAGTATA ACATAAGGTA AAC 333

5 (2) INFORMATION FOR SEQ ID :4:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :4:

AGGGAGAAAG GAACATCCGC GAACAGCCAA AGAAATCTCA GAAGAGTCCC 50
GGAGCTCAAG GATCAGAGTA ACACAATTTT CACTTTTCT GTCTTTATGT 100
20 AAGAAGAAAC TGCCTAGATG ACGGGGCCTC CTTCTTCAA CAGGAATTTC 150
TGTTAGCAAT ATGTTAGCAA GAGAGGGCAC TCCCAGGCC CTGCCCCCAT 200

25 (2) INFORMATION FOR SEQ ID :5:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :5:

ACAGAGCCAT TTGCATCCAC TGTGGTCAAC ATTTAGGAAG TTTTAAGCTA 50
AGATTGCCA AATTGTAGCC TACTGGATTC CGGTTCTCTT GACATCTCTT 100
40 TCTAGTAGCC ATGTCTTGCA CTTCCCGAGT ATAAACGAAC TGAGATGCAA 150

24

ATTAAAAAAA GGGAGGATTT AAGAATAATG AAAAGAGAAA AATCAAGAAA 200
GCACAATCAC TAG 213

5 (2) INFORMATION FOR SEQ ID :6:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :6:

CGCAGGAGAA GGAACAGAGC CATTGTGCAT CCACTGTGGT CAACATTTAG 50
GAAGTTTAA GCTAAGATT GCCAAATTGT AGCCTACTGG ATTCCGGTTC 100
20 TCTTGACATC TCTTTCTAGT AGCCATGTCT TGCACCTCCC GAGTATAAAC 150
GAACTGAGAT GCAAATTAAA AAAAGGGAGG ATTTAGAATA ATGAAAAGAG 200
25 AAAAATCAAG AAAGCACAAT CACTAGTGTA GAGATAACAG AATTTCTGAA 250
TTCCCTGAAA CAATCTATAT AAATGCATGT GAAATAATAC ACCAGCATCT 300
GTGGCCCATATA CGTCACATAT TAGGAACTGA TAACATAAGG TAAAC 345
30

(2) INFORMATION FOR SEQ ID :7:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :7:

25

TCCATTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50
GGGTTTTTTA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA 100
5 GCCCAATACA AAATATATAG AAAAAGCGAT TATTACAATA ACGCTTCAAT 150
TTCTTTTCC 159

(2) INFORMATION FOR SEQ ID :8:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :8:

20

ATATTTCAAT CGAACAAAAA GGAAACTTTT TTGAACTTA TTGAGGCTCT 50
ACTTAAGTAC ATCGAAACCC TTAATGCTTC TGGGGCTGTG TTGATTTCCCT 100
25 TGCCTGGCTG GGGGTTTGAT TCGC 124

(2) INFORMATION FOR SEQ ID :9:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :9:

CCGATACAAA TGTACGGAAT GTGTGAGTCC CTCTGGGAGC CCAACATGGA 50
40 TCCGGATCAC CTGTTTGAAA CCATCTCCCA AGCCATGCTG AATGCTGTGG 100

26

ACCGGGATGC AGTGTCAGGC ATGGGAGTCA TTGTCCACAT CATCGAGAAG 150
GACAAAATCA CCACCAGGAC ACTGAAGGCC CGAATGGACT AACCCTGTTC 200
5 CCAGAGCCCA CTATATATTA TTTCTACTTC ATCTATATAT TGCAAAAATA 250
GAAAATAGA 259

(2) INFORMATION FOR SEQ ID :10:

10

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :10:

20

GTCACCAAGA CCGAGGCCAA ACTGGGCACC TTCCCAGGG CCCTCAAGAA 50
GCTCCTGCAC ACAATAAAG CGCCCTCGTT CTTAGCAAG TCTGCTCCCT 100
25 CGAGGCCACA GCAAGCCGGC TACGGAGCCC CCGTTCTGTT TTGAGCCGAA 150
GACTACTTTA TTGGATGCGG TGAAAGGCCT CAGCTCTGAC ACTCTGATCA 200
CTGTGACAAG GGGCCC 216

30

(2) INFORMATION FOR SEQ ID :11:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :11:

27

5 CACACTTCTT AAGATACATC AAGTACTAGT GATCTTTGCT AGCAGTTATG 50
CCTGTTTCGT GTTACAGATT TGGCCATATA TTGACTAAAC AGCCCCTGTA 100
AAGTTGAAAG AAAAAGTTA TAACAGTGAA CTTCTGAGGT TTACGTTACT 150
GCAGGCTTTG TTGAGAAGAG ATTGTTACAG TGTGATTTAT GGATGATCAG 200
GGATG 205

10

(2) INFORMATION FOR SEQ ID :12:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :12:

TGCATCTGAA GAGTTGATGA TCGAGACTAC AGCTGCACTA TCAGACTGTC 50
25 AGGCAGCTCC CTCAGAAACA GCTTCAACAG ACTGGCTGCT GAGCAGACAT 100
CACCGTCCTT CCGAGCTCCA CGGCGACTCC ACTCTCGAAC TTCAGTCGAA 150
GTTGTTCCAC CACCTTCACG TTACCATTCA CCCTAAAAGA CCTTCTTGGG 200
30 TAAGTCCATG CTGCGTCAA TATTCCACTA TATTCCACAC TACTGCTGGA 250
TATGCCATTC TCGGTGA 267

35

(2) INFORMATION FOR SEQ ID :13:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :13:

5 GCCTCATCAG GTTTGCCCAG ATGCTGGAGA AGGTGTGCGT GGAGACGGTG 50
GAGAGTGGAG CCATGACCAA GGACCTGGCG GGCTGCATTC ACGGCCTCAG 100
CAATGTGAAG CTGAAC 116

10 (2) INFORMATION FOR SEQ ID :14:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :14:

TTCGAACTTA CCAGCATCAT GTTTGGTCTC TTCGTATGGT CAAACTTCAA 50
CTTTATAAAA ATAGTGAATA CCACTTATTG AGTGCTTAGA GTGTACCAGG 100
25 CATGGTGCTA AATACTCTCT ATCCATTATC TCATTAAATC ACATGACACT 150
ATGAGAAATG TACTATTCTT ATACCCACGT TGCCCAGGGT CATACATCTA 200
30 AGGGGTGCAA GGACCAGGCT TTGATTTCOA ATTATAATCT AATGCTCACT 250
CTCCAGGCCT GATGTCACGC AGCTCCTCAT TCTTATACTT AACATA 296

(2) INFORMATION FOR SEQ ID :15:

35

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :15:

CGTCAGTGTG CTACTTCACA TCATTAGCGA GGCCCAGAAA CTTGAACAGG 50
 5 AAGTCCGGCA CTACCAACAT GCCGCCACTC ATACAACTCA ACTCTTCCTC 100
 CAAACTCGAT TCAAAGAGCA ATA 123

(2) INFORMATION FOR SEQ ID :16:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :16:

20

CAACACATTA GTGCATCAAT ATGAATTACT TGTTTAAAAA ATCAAATGCT 50
 GGCATTGTCA GAAAAATTA ACAGGTTTAT TTATAATTAT CATAAAGTTG 100
 25 ACGCTGAAAC TTGTTCACTG AAACATTTTA ACTTGCATTA ATGCTTTACG 150
 TCTCCGCATT TATATTAAAA ATTCACACAC AAATGAAATG GAAAACTGC 200
 CAATACCTGA TTTCTGTCCC TATTTTTCAC TCGCAATCAT ATACTTAGTA 250
 30 CTTTGGACTC TA 262

(2) INFORMATION FOR SEQ ID :17:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :17:

5 TAGCCAAATT CTAGGGCATC CAGATGCATT TGAGCCAGTC GTAATCCAGG 50
AAATGTCAAA AAAGCCCCAA TGAATGAACA GAAAATAGCC AGGAAAAATT 100
TGAAAGTAAG TTTTGAAACA GGACTCGTGG AGATTCTAAA CCTTGCATTT 150
TCAAGAAACG TGCATCAGC 169

10

(2) INFORMATION FOR SEQ ID :18:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :18:

AGGGGCACCA TTACCATCCA TCTGACATCG CATTTCCATA GAAATGGCCA 50
25 AAGAAAGAAG GTCCTGGTAG GTTTTTCATA GAAAGACTCA AAAAGTTCAA 100
CCTTTGATGC TATGCCCCAG CCCAATACAA AACTACACAG AACAAAGCAA 150
TTATTAAAAT ACTGGCTTCG GTTTCCTTTT TTCCTTTGCA AAGTTTCCTA 200
30 CATATATGTC TTTTACAGTA T 221

(2) INFORMATION FOR SEQ ID :19:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

31

(xi) SEQUENCE DESCRIPTION: SEQ ID :19:

5 TAGGCTCTGT GACGGCATAG TTTTCAGTAG CTTTATCACA ATATTCACAA 50
TGGAGAATTA TATGACATGG TAGCAGAAAT AGGCCCTTTT ATGTGTTGCT 100
TCTATTTTAC CTGAAATTGT AGATATAGGG TAATC 135

(2) INFORMATION FOR SEQ ID :20:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :20:

20

GTTATCTATC TATCTTGACAG TTTACCTATC TGATCTGATC TCTGTAATTA 50
TAGTTCTGTC ATTTAAAATA TACTATTTAA ATCTAATTTT TACATTTCAA 100
25 AAATTATCTT CAGTAGTAAC TAAGTATATT TTCTGTGGAT TCTGAGAATG 150
TTATTTTTC AATGTGAGA GTACATATGT ACATTTATAA TCTTGTGACT 200
TTAAAGTCTG TTTTCAGATA CAGTATGTAA ATACTTGTA AAAAAATTGT 250
30 ATAATTTTGT GATAATGTAG TTTCCCAAAA CACATTTAGA AAGCATTATG 300
TTATTAGTAA ATGA 314

35 (2) INFORMATION FOR SEQ ID :21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :21:

5 TCTTCGCATC ACGCAGTACA GATACTCTTT CTGTACTTGC TTAATCTGCT 50
TTTTGGCATC AGTCAGTTCT CTTTCAGGTC AGCATAATCT TCTTCCTTCC 100
TCTGAAGATC TGCTTTCAGA TTCTGGGTAC GAGCAGAGCT TACAGAGAGT 150
10 TCCTCTTTCA ATATTTCTGT TTCTTGCC 178

(2) INFORMATION FOR SEQ ID :22:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :22:

ACATCTGATA TCCACCTCCA TGACAGACTG ATCACACCTC CTTCTATACT 50
25 ACTTCTGTTC TTTGTAAATA CTTAGTATTT TCCAAGGGAG TGTGAGAGAA 100
GAAATGCTAG GTTCATGAAG GGTCTCTAGG TTAACTTTC TTTCTTTTTT 150
30 TTTCTTAAAA CAACACACTT ATTATCTTAC AAATCTGT 188

(2) INFORMATION FOR SEQ ID :23:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :23:

TTCCANCTAA ACATCCAATA TNTCNTTTAN TGCTTTTATA TTTTNAAT 50
5 GTTAAAACCC CTATACCACC TTTTGGAAT GTTTTAAATT CTCCAATTT 100
TCGTTATATA GGATCAACCA ACTAAGAAA GATTTTATCA ATTGAATTGA 150
GG 152

(2) INFORMATION FOR SEQ ID :24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :24:

ACAATACAGA GGACAAAGAC CCCTCACAGA ATGCTTTTCA ACCAACTTCA 50
25 ACTTTTGCAC ACTTTTTCAC CGGTCCCACC ACA 83

(2) INFORMATION FOR SEQ ID :25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :25:

AAATGTCCAT TGCTGTATTG CGTGACCGTG GTCCTTGCCT GTCAAATNCA 50
40 ACAATGACCA AATGATGATG CGCCCTTAAT ACCAGGATGA GACCAAACCT 100

34

ACACATCTCC CAAGTGCCGA ACAAAAACCT GAACAAAAAC CATNTGCACC 150
CTACATCTGG CTGACATTTA CATTTT 176

5 (2) INFORMATION FOR SEQ ID :26:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :26:

AAATGTATGA TCAGAAAATA GGTACGCTTT TAAAATATTT GAACAGAAAA 50
GCTACAAATA AATNGAGCAA TGCTTTTAAA ATCATCTTTG TTTTATAGAC 100
20 TTTTCTCGC ATGAATTACA TTTTACAATT TCATNNGGCA TATTCGCACT 150
TTAAGTACTG ACGAAGAAGA CTAAACAAT CATTTTAA CAATATTTAA 200
25 AAGGATCATA TAGTCGACTT TTAAACANC CC 232

(2) INFORMATION FOR SEQ ID :27:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :27:

GAGAAAGTCC TTGCCATTCT AAAAGCCACC CCACTTCTCT AAGGAGAATG 50
40 GCCCAATCTT CCAAGTCCA CACAGGAGGG AACATTGTT TCGTAAATA 100

35

CGCAATGCAA AATTTNNTAT CTTGGCTTAA TACNNGACG TTTTATTTCG 150

AATGATGAGC CTTCTGCCCC CCCTTCCCCT TTNNNCTCCC CC 192

5 (2) INFORMATION FOR SEQ ID :28:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :28:

TAACACTTTA ANCATCTCTC CAAGCCAAGG AGGCTATGAC ANTGTAGCTT 50

20 TTATACTGTC CCCATCGGCC ACAATAACAA ACTTTTAACC CTCATAAAAT 100

GAATGAAATC ATCTTTCTAA GAATCTATAC CTACAATTCT CTGAACTAAT 150

CAATGAAAAA GATGATCAAT TCTGACTAAC AAAGATATAT CGATTCCATT 200

25 T 201

(2) INFORMATION FOR SEQ ID :29:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :29:

AACCTAAGGC AGTTGACCCC ACCTTCCAAC ATGTTTTTAC TTTATTGGCC 50

40 CCTCCCTACA TTCGGGTTAG GTTCCATTG ATTTGCACAA TAATGACTTT 100

36

ATTCTCTTT GATCAGGATT TGGCACATAA AATCCTTTTA TCATAGAACT 150
AACTATTTTA ATTACATATA ATGTAACATA TGGAGAGATT TATAGAGAAT 200
5 TTTGTTTTTT TGTCAATATAC TCCATTTTGA AGACAGATAT GATAGAACTA 250
GAAATTAAGT TGCATTTCTG CAAGT 275

(2) INFORMATION FOR SEQ ID :30:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :30:

20

GTAAATNTAC AAAGATAACG TCGCAATTTT CTTAGATTTA AATCAAAGAC 50
ATTCATCAAC AAGATTTTGA ATGGAATATT CCAGAAATTT CTGAGCCATC 100
25 TGATCACAAC AACCGTCTTT GA 122

(2) INFORMATION FOR SEQ ID :31:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :31:

GGATTGNAG CTTGAAGTTC AGAGCTGGTT TACCCAAAAA GGGAGCCAAT 50
40 AGAGATCTTC CCAATGAACC TCAATACAGC ATCGTAATAC TCGCACAATG 100

37

AAATGTTAAG TATGATTCTA GACTTCACTG ACTATCACAA TGATATTTTC 150

TCGATCGCAC TAGTGACAA CAAAACACGA TGAGTGCAAT GTGAAAC 197

5 (2) INFORMATION FOR SEQ ID :32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :32:

ACAAAAGTCT GAAGAAATCA CCAACNACAA GACGATTAGA AAATATGTTG 50

TTGGGGTCAC AACTAAAAAG TCCCTGATCT ACATTGNNTT TCNACTC 97

20

(2) INFORMATION FOR SEQ ID :33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :33:

CAAATAAAAC AANTNTTGTA AAGCTACAAT AGTTATATAC CAAAGCAATA 50

35 CCTATTACAT GCTTTACACA ATCCCATGAA AAAATAATTT AATAGCTCCT 100

AATCCCTGAT GCAAGGCACT TCAAAGCACC CGCACAAAAC TCCATGAAAC 150

AACATACAAT ACATCATTTA AATAACATAA ACGACTTTCA CACACTTGAC 200

40

CTAGGAAAAA ATAAATCCA TACAACCACA GCTAAAAACA TGTTAAGATT 250

38

260

CACAATAAGA

(2) INFORMATION FOR SEQ ID :34:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :34:

15 GGACNTGCCG NNNANNNANA GCCANTGAAC NCAGCCACCA NTGCAAGAAG 50
ACTGCCTCTT NCCAGGCAAG ATTTTACTGG AGCAACANAA CCGGAGGTGT 100
GATCCAAAAT ACCTTCCTTN CCAAGCCCGG GGTNNNNGAT AAGGTGTGGA 150
20 NTTNGGTTAA AGACAAGG 168

(2) INFORMATION FOR SEQ ID :35:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :35:

35 CTCGNACACT GTGGAGAGCC TGCGNNNNNN NNGGTNTACT CAGGGGGACG 50
AAAAGGAGNN GAANAAGTGA CACNGCNGNT AGCAGAGNGC ACAGAGCTGT 100
GCTNNNGTGG TCCCTTAGNA SCCGAGNAGG TGGGCGCGAG GTGAANAAGG 150
40 TGCNNGTGCG AGAGTGCGTG ATT 173

39

(2) INFORMATION FOR SEQ ID :36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :36:

AGCAACTNNN NNNNNNCATC CTGAAAGTCA AAATGGAATT TGTGTTTATA 50
CAACTAATAA TGATTTTAT TTGCTCAGTA CAGACTNATT TACAATGAAA 100
GTTTGTCTAA CCTTGTAAG CTTGTTTACC GTTT 134

20

(2) INFORMATION FOR SEQ ID :37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :37:

30

TGGCGCCTGT CCGAGAGCAA GTNGNNNNNN NNCCTGAAAG TCAAAATGGA 50
ATTGTGTTT ATACAACTAA TAATGACCTT TTATTGCTC AGTACAGACN 100
GATTTACAAT GAAAGTTTTG CTAACCTTGG TAAGCTTGTT AACCGTTTAC 150
ATGACTTCTT 160

35

(2) INFORMATION FOR SEQ ID :38:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs

40

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :38:

CTAGTTTAAT GAATCTGAGG GGCTACTATA AACAATCCCA CCCTCACACG 50

10 ATTTTTTACC TTCNTTACTT NGCCCTTCAT TAGGCAACCC TAGCAGCACT 100

CCACCTCTAT TCTCGCACTG TCCAAGAGGC CCACCTAATC 140

15

(2) INFORMATION FOR SEQ ID :39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :39:

AGCAAGTATC ANNNNNNNNN ATACATTGA ATTCAAGTTG TTTTGTGCA 50

AATTGTACAG TGTGTCAATT GATCTTCAAG CTGNNGGTGC CTAGAAATGG 100

30 GNCGGTGTCT GTAGCCCTGG CATGTGCACA CGGAGCATTT GCCACCACCG 150

CAAGCAAAAA GTCTGGGNGA AGTTCACCAA NGNCAAGAAN NATTANGGGA 200

35 AAA 203

(2) INFORMATION FOR SEQ ID :40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

41

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :40:

GAAAAGCNNN NNNNNNNGGC TTAAAGAACA ATATGCTGAG ATGGAGAAGG 50
ACCTAGCGAA ANTNNNAACC TTTAAGAAC TTGAANNACA ACAATCACAA 100
10 ACTAATGAGA AGATGTTTAC CTCTCTCCTG AAAACTATGC CCACCAGACC 150
GTTTAGCCTC TGCTCAAGCT 170

15 (2) INFORMATION FOR SEQ ID :41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :41:

GCTGCATGTT TCCTGNATT TGAGCTTGAA AGTTCAGAGC TGTTTACCCA 50
AAAAGGGAGC CAATAGAGAT CTTCCCAATG AACCTCAAAC ACGTCGTAAT 100
30 ACTCGCACAA TGAAATGTCA AGTATGATTC TAGACTTCAC TGACTCATCA 150
CAATGATATT TTCTCGATCG CACTAGGCAC AACAAAATAC GATGAGTGCA 200
35 ATGTGAAACA TCTACAAAGT AAATCACACA CTGTTTTTTT AAATNCATAG 250
AAATTGATT TGTAATAAAA 270

(2) INFORMATION FOR SEQ ID :42:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

42

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :42:

	AGAGCTGCAT GTTTCCTTGA TTTGNAGCTT GAAGTTCAGA GCTGTTTACC	50
10	CAAAAAGGGA GCCAATAGAG ATCTTCCCAA CGAACCTCAA TAACGATCGT	100
	AATACTCGAC AATGAAATGT TAAGTATGAT TCTAGACTTC ACTGACTATC	150
15	ACAATGATAT TTTCTCGGAA TCGCACTAGT GCACAACAAA ATAGATGAGT	200
	GCAATGTGAA ACAATCTCAA AGTAAATCAT ATACTTGTTT TCTTA	245

(2) INFORMATION FOR SEQ ID :43:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :43:

30

	TACACTGNGA AAATGTACAA AGAAAGTATC CCCAAATNAT TTACAAAGCC	50
	TAAATGTCCT TGATACACAT ACACGGNAGT ATGCAGACAA CAAAGATTAA	100
35	ATGAAGACAC TTTTACTTT TCGG	124

(2) INFORMATION FOR SEQ ID :44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :44:

GAGTTCTCAC GAATACACAG GTTCAGAGAG ATGAGANGGA ANAACATAAG 50
GCAAATTCCT AACANNCGCT AATATAGGAG GCCGCTCGAT AGGATTTTAA 100
10 AAAAATAAAA ACAATCTTAA TAGTGGGACA AGGCCATCAG AAAA 144

(2) INFORMATION FOR SEQ ID :45:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :45:

25 ACTGATTCCNN NNTGAAAATA CCCCCTTTCT CCATTAGTGG CATGCTCATT 50
CAGCTCTTAT CTTTATATTC CAGTAAGTTA TTTTGCTCTC ACTGTTTTAA 100
CAAAAAAAAA AACACAACA TAAAAATCCT TGCAAACCAT GTCAATTGGA 150
30 GAAATTTAAT GTTTTTCATA ACATGAA 177

(2) INFORMATION FOR SEQ ID :46:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :46:

ACTGATTCTG CGAAAATACC CCCTTTTAT TAGTGGCATG CTCATTCACT 50
 5 TTATCTTTAT ATTCAAATAA GTTATTTTCG TTTCACTGTT TTAACAAAA 100
 AAAAAAAAAA AAAAAATAC AGCCCTCCCC AATCGAAGAT TTCAACTTTT 150
 TAATTCACAC GGAAAAACCA AGACAATTC ACAACTTCTG GACACAACCA 200
 10 TCAACACAGG ACATTTTTTT TACAGGCAAA TCACTTAAA CAAAAAGAT 250
 CCCAGA 256

15 (2) INFORMATION FOR SEQ ID :47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :47:

GAGAAAAGTC NNNNNNNNA GGTAACTA ACTTTTCTTG CTTATTTTCA 50
 CTATGATCTG AAAGGATGGA AGACACAAA TGTATGNNTA AGGTATTTTT 100
 30 AACAAAGATA CATGGGTAAA TTAACAGCAG TAATGTAAA AAGACTGAGG 150
 AGCAA 155

35 (2) INFORMATION FOR SEQ ID :48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID :48:

5 GCTTATTTTA CTATATCTAA AGGATAAAGC ACAAATGAT GAATAAGATA 50
TTTNNACAAA GATACACG 68

(2) INFORMATION FOR SEQ ID :49:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :49:

20 CCTGAAAGCA AAGCCATNNA AAGCTTAGAG ACAAGCACNT GAGATGCAGG 50
GGCCTAGCTA AATTNGAAC CTGNTGGAAC TTGAACCACA ACGATAAAAA 100
ATTACAGAAG AGTTCACCTC TTTCTGAAAA CTATCCACAG ACCGTTTACC 150
25 TCTGCTTCAA GCTANCAATA TATCAATGGC ACTCTCATAN CAGAAGAAAG 200
AAGTTCCTAC TAGCTCCTGA TTATATTNAA GAAGATGCCC ATGG 244

30 (2) INFORMATION FOR SEQ ID :50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :50:

ACTCGNNCAG CGATAGTCGG AGCTCACCAA CAAAACNCT NNNNCAGAAA 50

46

GGANAAAGNG CCGCCCTACG TGGTACACAC A

81

(2) INFORMATION FOR SEQ ID :51:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :51:

15 GTACTTACTG CACTATGAAA AGCAATAGAT CGTCCATAAG TTATAACCAA 50
AATCTCTCCC TCAGGAATAT ATTCCATACT ACTAACAGAC ATATTAAAAT 100
TTAGAGATTT CACTTCTGTC ATAGTAGCAT GATCCCAAAG TCGAACAGTT 150
20 TTGTCATCAG CAGAAAGAAT CTGTTTATCT CACTGCACCA CAGAGCTTTT 200
TTATACCAGA AGNATGACCA CTG 223

25 (2) INFORMATION FOR SEQ ID :52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :52:

TATGGTTTNT TGTA AAAAAG CTCANNNANA AAGGGANNNGG CTTAAGAGA 49

(2) INFORMATION FOR SEQ ID :53:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs

47

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :53:

CAACGTCAGA GCACACNNNN NNCTCAGNGC ANAGGCATGA CAGGAGCTCA	50
10 TANCNATAAG CCATATAANN NTGTTACCTG TATAGAATGA TGAATTATCT	100
TTCTAGAGTC TATACCTACA GTTCTCTGAG CTAATCAATG GAAAAGATGA	150
15 TCAATCTGAC TAACAAGAGN AATTGATTCA TTTTCTTCCA CNCCCCTTCA	200
TTCAATAATC AAA	213

(2) INFORMATION FOR SEQ ID :54:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :54:

30

GCGTGTTGTG NGGAGTGGNN GTCTNGTCNT CCTGTTAAGG TTTTGTGTG	50
CGTNNTTGCG TANGGGGNGG GTTTNGGCAG GTGTTGCCGG TAGCNAAACN	100
35 GTTGGCCCCA TNGCCNGNAT TGNNNCCCN CNNGGGAANG GGGGGGNGA	150
CCNNAGNGGG AAAAAA	166

(2) INFORMATION FOR SEQ ID :55:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs

48

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :55:

ACCTCATAGC GAACTCGTCN TATAGANNNN ANNTGAGTCG AGCTCGATGT 50
10 NGNCGTTGTN GCTGCCAAGC GACAT 75

(2) INFORMATION FOR SEQ ID :56:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 181 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :56:

25 AATNNNNNCC TATTTTGTA TTTTGTGAA AAAAGTTCAA TGTTCAAGTTT 50
TCCTTAGTTT TTACCTGTT TTCTCTATAG GTCATGATTT CTGTGAAGCA 100
AAAAGATGCC TTTTACCATG AATTCTTGAG TTTACATCAA TAATATTGTA 150
30 TATTAAGGGG ATCAGAAGTA GGAAGGAAAA A 181

(2) INFORMATION FOR SEQ ID :57:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :57:

TCGAAGAGAC CTCAATCACC GTTTTTCAGG ATGTTTGATC ACAATACGAA 50
5 GATGACGNNNA TCCAATTTCA GAACACCACA GGGCACTGGC ACACAGAGGG 100
GATTATTACA GAACCACTGA GATGACATT 130

(2) INFORMATION FOR SEQ ID :58:

10

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :58:

20

GTNATTTTGA AGGTCTCACA AATNTAAAGA CTTATTGTAG CCCATGAACA 50
CATTGACAAG TACAAAAATT ACAAAAATAT GCAGAAATAT TGAATAACTA 100
25 GAACACAAGC CACTGTTTCA ACTCCAGAAA AAAGAAAGGC TTTACTTTTT 150
CCATGAA 157

(2) INFORMATION FOR SEQ ID :59:

30

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :59:

40

GAGGTGAAGT TGTCTTTTAT TGAATTGCAT TATNAATGNA TAGGCTGTGC 50

50

CTTTTGNAC TCTCTATGAG TTCATGAATT TAACCAATAC GNCCACAAAT 100
GCTGCTGCTG TCACAGAGAG ATGCCGATAA AGGACACCCA CCACCAATTT 150
5 TTGAACAGGG AGGGGAGAAT CAACTCTGAA TGTGATGCAG TGACCAGGAG 200
AGAGGACCAT GTTAACAACA CCACACAAAT GCAAATGACT NGTTCTNAAA 250
CA 252

10

(2) INFORMATION FOR SEQ ID :60:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :60:

GACCTCGTTT TTCATCCTAT TATGGCGTTT ANCAGGCTAG ACAGAAACAC 50
25 GCCTTAACTT TANTTGCCAC AAATCTTAAT ATTTTCTCCA CTAATATTAG 100
AAAGGAAGCA ACAAATAATG TCGCTTTTCA CCTGACGTCT GGTTCAACTT 150
TCCGCCCAGC CTATTCCTGN GTCTTCCTCC TGCCTTTCTA ATGTCCCA 198

30

(2) INFORMATION FOR SEQ ID :61:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :61:

51

GAGGTGGCAT TATGTGAGAC AGCATTGGT TAGGGAGTGC CAAGCATTCT 50
 ACAGCATTG ATGGTGGAAA TAGTCATGCT TTTTATTTCT GCTCTCTAGG 100
 5 AATGTAAGGT GCACAGCAGG TCAGGGTACT GCTGTGTGAG ACAAAGGTC 150
 CAGGTAGAGG CAATCCCCCA GATGCAGGCA GGGCAGGTGC TCACTGGGCA 200
 GAGTGCTTCT CATAACCTT CAGGAACCC 229

10

(2) INFORMATION FOR SEQ ID :62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :62:

CATCCTGGGC CCTGGCCGAT GTGCATATCA ACANAAAAAA GGGACTGAAG 50
 AACATCGGCC ATATCATCCA CACAAGCCAA ATCTCACACC TTTACTTTAA 100
 ACCGCTTAAT GAATTCATG ACCTTGAGGG CTAAAGATCG TTCTTCGGGC 150
 AAGAGCTTTT GGACTGTTTT TAGAACAGAA T 181

30

(2) INFORMATION FOR SEQ ID :63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :63:

52

GTTGATTGTG AATCATCCCT CTAACATATA ATCAANANTA TGACTAGAGA 50
 ATTTGGCAGA AACAGAAAA GGACATGGGA TAACTTTTAG ATTTAAAGAG 100
 5 GCAGGCTTGG AACACAAACT GGTATTCTGC TGACACACTG CTGCATATCA 150
 TAAGGCTACT CCACAAGACC ATTAGAAGTC 180

(2) INFORMATION FOR SEQ ID :64:

10

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :64:

20

ACAATGTTCC AACATATATA TGGGGAGGGG AGAACANTTA TCTGTATAAC 50
 AGGGAACTGT GATTATTTAA AAATANGCNA GAACTTATTT CANCTGTGCT 100
 25 TTAGAAANAA NTGTATACGG 120

(2) INFORMATION FOR SEQ ID :65:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :65:

40

CACATCGCTA TAATCCTTTC TGAGGACTTA AACTTTATN CCACTTACCT 50
 TTATGACTTT TAACAAGCCT 70

(2) INFORMATION FOR SEQ ID :66:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :66:

TTTCGAGCAA AATGTTTACA TTTACATGGA AATACACACT AAAACAGAAT 50
15 ATTTTCCTAA TCATGAAACT TCGCCAAAGC AAAATACAAA CTTCCAACGG 100
GAGGTCCACT CAACTAACAA CAATGATCCC CAAGCAGGGC ACCAAGAAAC 150
CTGGGGGACC CTTTNCAAAA AACCTCCTTT CAAGAGACCC TAATACTCTN 200
20 TCCACACACC CACACGATTT AGGAACTTGG ACATGTTCTT 240

(2) INFORMATION FOR SEQ ID :67:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :67:

35 GGAAGCACTA CATTTTCATCC AAAGCTGGGT TGAGTTATTT TTGAACACTT 50
TACGATATGC TTAGGTAGGC TTTTAACTTG CTCCTCCAAA CAATATCTNT 100
TGGGAAAACA AGCCCTGTGG AGAGATCCTT CCATCAAGTC GCTTCAATTT 150
40 AACCTATTTC TAGAGGACTA GACATGCAGA ATCGTCAACT ACAGGGAATG 200

54

AAAAGTTCAA AAAGTAGATC CTACAAGATG AACGAGTACT TTTCTAAACA 250

TAAG 254

5 (2) INFORMATION FOR SEQ ID :68:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :68:

AGGCACCAAA GAAACACCAA GCAATAAGT GAAAGACTAA CCAAGATTTG 50

ACATTGTATG NTTACTGTAT TCTTTAAGAA ACAACTACAA AAAGAAAATG 100

20 TCAACAAATN NNNACAACCTG AGAACCTGGG AATCCCGCA CGGAAGACAA 150

GAGATAACCT CTCCAATTTA ACACCGCTAG GNTTCTATNN TA 192

25 (2) INFORMATION FOR SEQ ID :69:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :69:

AGCAGCGNNN NNNNTNNAAG CAAAAGACAG GAGCAGAGAG GCCTGAGAGC 50

AGGAGGCGAA TTCGATCTCT CCTCACAAAC AGCCCAGGAA AATATACACC 100

40 CCGGGGGAAG CC 112

55

(2) INFORMATION FOR SEQ ID :70:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :70:

AAGGGTCTCC AATTTAATCC TTGGGTTGTT TTACCACTTC TTTCGTAAAT 50
15 TTATCAAGAT TTCTTTCGCA CAAATACTCT AGCGCCTCAC AACAAACCTG 100
ACCTTGCGCA GGAAGTCGAC CATCAGCACC CCCTTTACAA CATCGTTCAT 150
ATCACAATTG AGAAGATGAT GAATGAAGAT TCGCTTCCAA GTTCCAAGGG 200
20 CAGATTTATT CCTTTAACTG ACATTTCCAT GA 232

(2) INFORMATION FOR SEQ ID :71:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :71:

35 CNTGGATCCG NCCTTGTTAC GNCCAGGACG NCTGGACCGC AAAATGAATT 50
TTCACTTTTC GACCACCGCC AGAAGAGATG ATTTTCTCAT CATNAACAAG 100
GAACCTTTGA GGAGATCGAC TGAAAGACTA GCGNCCCNGT CAGATAAGAT 150
40 TTAGGGCTGA 160

56

(2) INFORMATION FOR SEQ ID :72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :72:

AAGGAAGACT GGTTCGCCAT CCGAGATCAT TAAAAANGNC TGACCCTAAC 50
AATACGTACA AAAATATAAA ACGCAAATAA AAAATACAAA CAGATTCCTT 100
CTTAAAGTAC TTTTAAGAAA AAAAGCAGGN CCTTGGAAGT TTCGATTCTT 150
TTTTCTCCC GTCGCAAATT CTATGTTTGG AT 182

20

(2) INFORMATION FOR SEQ ID :73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :73:

CAAGAGGCAG CTGCCCTCC CACCTCGGAG GNCTGAGAGG GNCTGTGNCG 50
ATGAGCTGGA CGAGCACAGC ACTAAAAAGG CTTGCCCTNG CACAATAACA 100
CTGAGAGGAT GATGAGAACA CNCTTGAAAT GCTTCATNCA CATGGGCAGG 150
ANAGGCTGCA CAATGAAA 168

40

(2) INFORMATION FOR SEQ ID :74:

57

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :74:

10

AACCTTTATT CATCCTCCTN TCCAAGACCT ATGAGAAGGT TCCAGGCCCC 50
AGGAACACAG GCTTCTTGGC CCCAGATGCA CCTCCCTGCA CCCCggggTT 100
GTATACCACA CCCCggggCCC CTAATCCCAG GCCCCGAGAT AGGAAAGCCA 150
ACTAGTTCTT TNTNTGTGAT TCAGTAGGCC TGACCTATAG NTGGAATGTC 200
NCTNTCCCTN NAATAAATTN C 221

20

(2) INFORMATION FOR SEQ ID :75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :75:

AGACTGNTTG GGTCAATCCGA GATCATTAATA AATGNCTGAC CCTAACAATA 50
GGCACAAAAA TAAAAACGAA ATAAAAAACC TCCTTANNTT CGAAGTATCT 100
TAGAAAAAAA CAGGGCCTTG AGTTCTG 127

35

(2) INFORMATION FOR SEQ ID :76:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs

58

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :76:

AAAAGAACAG CAGTTTCACA TTTCACATAT TTGAAAAACA TTTCAAAACC 50
10 CTCTAATAAG TATTTAATGA AAATAAATTT ATCGAAGAGA AACAAATGACC 100
ACAAAATTAA TACTACCAAA TCATTACTGA GACTCTTGCA TTACAATATT 150
15 TGGAGAGTAG GTGAAGAAAA TTAGACCGA 180

(2) INFORMATION FOR SEQ ID :77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :77:

GATTAANNNN NNNGCACCCN NNATTACTGG CACAGCTGGT GAATATTTTC 50
30 GTGGACTTTT GACTAGTGCA CCTGCGTGCG GGAAAACANT GATAAACTG 100
TCACTTTAGC CNCNACTAC AAGACCNGTT AGACTAGAGA GC 142

35 (2) INFORMATION FOR SEQ ID :78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :78:

5 GGCCTGAGA GCAGGACGGC GAATTCGATC TCCTCCTTCA CAAACAGCCC 50
ANGGAAANTA CACCCCGGGG AANNCCCCNC NCNNTTAGAA CCNNCAGGNT 100
CTGNCCCCCC CNNNGNCCCC CCG 124

(2) INFORMATION FOR SEQ ID :79:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :79:

20 AGGTATAGTG TTCCCTAATC ATGTACTTGT GAAGCACCCG GANTTTTTC A 50
TATAGTCTAA AAGCTAGAAG AACAAGAGTG TATTTCTGG GTGGATGTAT 100
25 NGTCACTTGC TGAANNNTT GAAATACCAT TATCCCCCTT GCTAACNCCT 150
TTAAGNAAAN GCCNTTTTAA G 171

(2) INFORMATION FOR SEQ ID :80:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 98 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :80:

40 CTGAACAGTG TGGTCGAGCA TTCCAAGTCC GTGAAGGTGC AGGAGCGGTA 50

60

CGACAGTGCC GTGNGGGCAC CATGGCACCT NGACCACGGG CNCCTAAG

98

(2) INFORMATION FOR SEQ ID :81:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :81:

15 CCTCAACAAG TGCGAGACCT GGGCGTCCAA CCTGCCTACA ACCACAGCCG 50
CGAAAGAAGA AGACCTGCTG CTTCAATACA ACACGGGAGG ACCTGGCCAT 100
CAACATCA 108

20

(2) INFORMATION FOR SEQ ID :82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :82:

ACACATNACC CACNGCCAGT ATATCTCGAA CAAAGTCTCA GACGATACTC 50
35 CCTAAATTG TAAAGCTTAA TACAGGTTNT GGAAATCATT TAACACCCGA 100
GAATGTCCCA TCACAGTCTT CCGTCAAAAT TTAGCCTCAC AACAACAACA 150
ACGCCTACGA AATTCTAAAT TCAGAAGGAA 180

40

(2) INFORMATION FOR SEQ ID :83:

61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :83:

10

GGCTTCTGAT CGCCATCCTT GAACAGGGCA AAGGTGGCCT CACCAGCCTT 50

CGATGCAGCT GCCATGCGCG CCAGAATCAG CGAAGGCATA CCCTTACGTC 100

15

GTTGGACGCA TGTTTAGATG CCTTTGAGAC CGCCCAGAGA AGTCCTTGTC 150

CTTCTTAATA AACACCTCCT CGCCAACGTC GACGACCACA ATCACCGTA 199

(2) INFORMATION FOR SEQ ID :84:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :84:

30

CTTCGGTAGT GCCGCCGTGG TGCCACACAC CGTTGAGGTT GGAGTGGGCA 50

CAGGCATGGT ACCACCAGCC TCCCCGCTGG TACAGGGCAC AGTTACCTGA 100

35

GGGGAGAGAG AGAGTCCATG TCCTCTCACC AGAATAAAAG CCTCTACCTG 150

CACCTCACAG TGCAAGGCTT TTGCCAGGCA TCCCCTGGCC CCTCCCATT 200

NACNGAATAC AACC 214

40

(2) INFORMATION FOR SEQ ID :85:

62

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :85:

10

CCTGGGCAAG CTGAATGTGA AGTTGACCAG GCTAACTGAG AAGCAAGCCC

50

AGTACCTGGG CATGTCCTGT GATGGCCCCT

80

15

(2) INFORMATION FOR SEQ ID :86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :86:

GGGGATAGCT GGCTCATCCT CGGAAAACAG ACCCACATCT CTATTCTTGC

50

CCTGAAATAC GCGCTTTTCA CTTGCGTGCT CAGAGCTGCC GTCTGAAGGT

100

30

CCACACGGCA TTGACGGGAC ACAGAAATGT GACTGTTACC GGATAACACT

150

GATTAGTCAG TTTTCATTTA TAAAAAAGCA TGACAGTTTA TTACTCTGTT

200

35

TCTTTTAATG

210

(2) INFORMATION FOR SEQ ID :87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

40

(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID :87:

5

CACAAAAAGC ATGATCAGGG CTAGCCTCAA TACAGGGAGA AATCATGGAT 50

ATTAAAAAT ACTTTTTTTG ATTCAGATTC CGGTATGACT GAAGANGCAA 100

10

CA 102

(2) INFORMATION FOR SEQ ID :88:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :88:

25

GATAGGCGCA TGCATACTAC GGCTAAGGAG AAACAATGTT CCTACATATT 50

ACGGGCAGTG AGAACATTAT CTGTATAACA GGAAGTGTGA TTATTTAAAA 100

ATAGCAGAAC TTATCNGTCT GTGCTTTAGA AATAACTGTA TACAGTGTTA 150

30

TAAGTTGAAA AGAACTCAAA ATAATAATA CAAATAAGAA CCTACGTATT 200

AGAATTCAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA 250

35

TGACACAAAT TCAAAACACG ATCAT 275

(2) INFORMATION FOR SEQ ID :89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

64

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :89:

GCCTGATGGT ATATACTGTT TTGCAATTGC ATACAACTGT GCATTACAAA 50
TTAATAGTAA TTATGGTTTG GNNGTAAAT CGAGTTTCAG AATAAAATNA 100
10 AAAACAATAA AATCCAAAGA ACGATGTAAA CAAAAAGCT TTTGTTTGT 150
TACAAAGTAT ATTAAGGATT TTCTGCTAAG ATTCAGTTTA AGAGTTTCC 200
TCGTGAAAAC TAAGTAGAAA CACAATGCCA ACAGCTGGCC AGTAATCAGT 250
15 GCTGTGTACT CCA 263

20 (2) INFORMATION FOR SEQ ID :90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :90:

30 GCGTCCTGCC CAACATCCAG GCCGTACTGC TGCCCAAGAA GACGGAGAGC 50
CACCACAAGG CCAAGGGCAA GTGAGGCCGC CCGCCGCCCC CGAGGGACCC 100
35 CTTTGAGA 108

(2) INFORMATION FOR SEQ ID :91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double

65

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :91:

GCCTTGGTGG AGGGCATGAG GCTATGATGA CTATTGGCTA TAATATGGAT 50
ATGGCTTTGG CTGATAGATT TGAAGAGACC TCAATTACGT TTTTCAGGAA 100
10 TGTTTGATCA TAGATACAGA GATGGTGGTC CAGTTTTCAG AGCACCACAG 150
GGCACTGTGT ACACATGAGG GGTACCTTA CAGAGCCACT GAGAATATAT 200
15 TAATAA 206

(2) INFORMATION FOR SEQ ID :92:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :92:

CCTTGGTGGA GGGCATGAGG CTATGATGAC TATTGGCTAT AATATGGATA 50
30 TGGCTTTGGC TGATAGATT GAAGAGACCT CAATTACGTT TTTTCAGGAAT 100
GTTTGATCAT AGATACAGAG ATGGTGGTCC AGTTTTCAGA GCACCACAGG 150
35 GCACTGTGTA CACATGAGGG GTTACCTTAC AGAGCCACTG AGAATATATT 200
AATAAANNNG 210

(2) INFORMATION FOR SEQ ID :93:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs

66

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :93:

AGGACTTCAT CCCAGACTCA CTTGTTCTGT TACAGAACT AACCTAAAAG 50
10 GCTGGAAATT AAAGGATACA ACCTAAGAGG TTATAACAGC AGACTGGTAA 100
AACATGGCGA AAGGAGCTCT CTCTTTCCCC GCAGTCTACC AAGCTCCTGT 150
15 GCATTTTCAC CACATAGATC TGCTAGCTTA CAAATGATG 189

(2) INFORMATION FOR SEQ ID :94:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :94:

GAAGTGACAG GNAAGCTACA GGTGTATAAC AAATTTGTAA ACTAACCAAG 50
30 CACAATGTGG CAGGGCCTAG CTGCTACAAA GAAGACAATT TAACAAATAC 100
TCAACGCATG ACAAAAACT CAGGACTGCA TTTGCACTAA TCGATAACGN 150
35 GTCATTTAAT 160

(2) INFORMATION FOR SEQ ID :95:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :95:

TGCTTTATAC ATNATNAAAG GTAGGCACTT CATAAAATTT GCATTTTGGT 50
AAAAGGCAAC AATTGATGT CAGTATCTTA ATTGTGTCAT TAACTTTTTT 100
10 AAGAGAACAG ATTATCAAAA TTTTACGAAG AAGAAAAAAA NTATAGTTTT 150
TAAGGAAACT ACAGAAGGGA T 171

15 (2) INFORMATION FOR SEQ ID :96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :96:

GTGGATAAGA AGATGTGTAC TTGGGAACAA GGCTAAAGCC ATTGGCTGAT 50
TTCCCAACC TTTTATTCG CGAAGAACT CCAGTTGTTA ACTTTTGTAG 100
30 AGTTTTTTTT GCAAAAGAA CTNCATTAN C 131

(2) INFORMATION FOR SEQ ID :97:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :97:

5 GTCCCTAATAT TTCTGTNCAG AAATTGTCAA CTTGACTTGA GAGTTGAGAA 50
 GTAAAGTTAA GGCAGTGACA ATATATCAGA ATGGAAGTCC TTAAGAGCAA 100
 CTAACAGGTT CTTGATCAGA CTGACTATCT TTTCTTAAGT TCATAATATN 150
 TTAAGTGTCCA GCCAACTATA CTTGGATCAA AATATCCTTC ATGAAGGGCC 200
 10 ATAATGTATT GATGATCTGC TGTAACCTTG AGAAGCTTCC TGAAGCTCNT 250
 TTTGAATAAA TTTATNGAAC TTATGAAGA 279

(2) INFORMATION FOR SEQ ID :98:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :98:

25 GTGAGTCTTT CTTCAACTAG GGGAAATGTTT CCAGGGCAGC CCAGGCCTCA 50
 CTCACGCAGG CCTCCGCGAC AACTGTTCAG CACTGACTGA GGATGAAGTG 100
 30 AAATCCTGAA AGCTGAGAGC CAGCGCCCTC ACACGAGGGC TGGGACGTAA 150
 CAAAAGCCCA TCAAGAGTTT TGCCCAGGGC TTTCTTGAGC CTTGAAGCAT 200
 35 GACGAGACCA GGACCCTTTA GGATTAAGCA AGTTTTATGC GGTCTNAAAA 250
 AACTCCAGGG CCTCCA 266

(2) INFORMATION FOR SEQ ID :99:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 base pairs

69

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :99:

GGGAACATTT ATTGACATGA AAAGGTGTTT CAGATATACT GATATGTCAA 50
10 ACAAATAGTA AAACAACATA GAGTAATGAT TCATTTTGGT AAAAAATATA 100
TATGTATATA TAGAAAAAAA TTCTGCAGGA CATATGCTAA ATTGGTAACA 150
15 GTGCTTACCC CTGGGAAGGG GGTATACGAT GTTGATTAC TCTTTGGGTA 200
CGTATT 206

(2) INFORMATION FOR SEQ ID :100:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :100:

30

CGCAACTNTC NCTAAACATC CAGTTTTCTA ATNTAATAAA AAATGGCAGT 50
AATTATCCTC ACCTCTCAGG GAA 73

35

(2) INFORMATION FOR SEQ ID :101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :101:

GAGCACAATC ATGNGCAAGC GCAACAGCAC ACCTTTATCC GAGTGAGACC 50
 5 ACTATGCAGC NGAACAGAGA CTTCTTATCT CTTCTTCTTG ATACTTGAAT 100
 ACTGCCCC 108

10 (2) INFORMATION FOR SEQ ID :102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :102:

GAATTATCAA ACCATCNTTG CTGACATTAA TTTCCAGCT TTGATCTTAN 50
 NTCTNGCTTT AGTCCTCATA CAATGACTGT GTTTTCTCA AACGATNTAT 100
 25 CGTATAGGNA TCCTTCTAAG CAATCCTGCA CCCACAAAAA AGCTGCATCT 150
 TCAATATAAC ANAAAAAGGN ATTTTGCAAA AAGTACAAGT TTTATGTCTN 200
 30 CTGTAACTG 210

(2) INFORMATION FOR SEQ ID :103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :103:

71

CGTAGTTCGA TTCGAGTGGT CTATACAATC ACACCAAGCT TGATGTTGAT 50

GTCACCAAAA TTTCTTTCCA AAAAAA 76

5 (2) INFORMATION FOR SEQ ID :104:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :104:

CTTATGATTA ACTAAGCAAA TCTTTCATAG AAAGATATTA TCAAAGCTGA 50

AGAAATGCAA ACTTNAACAA AGTGCCGTGA GATTCCGGAA AAACCCTTAA 100

20 CCGATTGAAT GGTTTTTTAA GAATAAAAAA GAAGTCTGAT ACTGAACTAC 150

AAGTCGCAAG GAACATC 167

25 (2) INFORMATION FOR SEQ ID :105:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :105:

TATCTGCATA TCTAACATA GAAAAGCACA ATAAAAACAC ATATCATAAC 50

CTCACGGGAC CACCATCATA CAGCAATTG TCATGATCAA AAGAAACATC 100

40 ATTAGTCGTG CCATAACTGT AT 122

(2) INFORMATION FOR SEQ ID :106:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :106:

GAATTCTTCA CTCCAGATTT CCAATGCCAA GATACATTGA TACTGAACAT 50
GGAGGCAACC AGGCCCGTTT CCTCCTTTCA AAGTCAACCC TCACAGACTC 100
ATAATAATAT GCATGCCTGG GGGCAGGAGT CTGGAGCACC TATTCTNACA 150
GATGATGTTA TTTACAAGTG TTTATGGATC ACTTGAAGAA ACTTGCTGTG 200
TCCAGTGCTG CTTGAAGTGC TAATAATGTT AAAGACACTT AAGAAGATGA 250
AATAA 255

25

(2) INFORMATION FOR SEQ ID :107:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :107:

GGACGTGAAT TGGTGAATA TTTACAAAGA AACTGTTTT CTCAAAACAC 50
TGTTCAATTGG TTGCAAGAAT GAATACTGAC TTCAGAACTC AAACAATGGA 100
AGAACTTGCA TTTTATGGA ACTCAGTATT AAAAGAAAAT ATAATGTGAT 150

73

AGCACTTTGC AGATATGTCT AGACTGTGAT CTGAAGCATC GTAGTTTCCT 200

ATACCAAGAN ACANTTATGT GGTAAT 227

5 (2) INFORMATION FOR SEQ ID :108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :108:

GAAAAATNGC ATGAAAGAAG ACTCTNNNN NGCCATACCA TGGTACAATA 50

ATCATNAAA NACAANAACA AAAACAAACA CATAAACCA CTCACATATA 100

20 CATGTAGATA CAACAACNAT ATAATATCAA TAAAAAAA ATAGNAAAA 150

AAAAAATAA CA 162

25 (2) INFORMATION FOR SEQ ID :109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :109:

AATTAAAAAT ATTAAACAAA ACTACCACTC CTCCTTATTA AAGCCCATAA 50

AAATAAAAA CGAAACCCGA GAACCAAAT GAACGAAAT CTTTCGCTTC 100

40 ATTCATCGTC CCCACAATNC CAGGCCTACC CCCCATCTG ATCATTCATT 150

GTTT

(2) INFORMATION FOR SEQ ID :110:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :110:

15 ATGTGCCAAG TAAAAAATCA ATTNGTNGCC TTTTCCATT NCGCGGACAC 50
CCATAGGCAC CAAAAAAGG TGCTAATAAG TAACATGTTT TAAGATGCAG 100
AATAAGCTAT GGAAACAAGG AATGCTCCAA GTGTCCAGT CTTTCTCCTT 150
20 GCACTCCTTG TTAATAACAA TACACTATAT CA 182

(2) INFORMATION FOR SEQ ID :111:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :111:

35 GAAGGTGAGA ATAGGCTAGG GGAAACAGTA GGACAGGAAG TATTCACGTA 50
CNTCAAACC AATGGTAGAA CATCACATTT CAAACTGCAA ACCA 94

(2) INFORMATION FOR SEQ ID :112:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs

75

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :112:

10 TAGGGCAGTG AAACCTAATC TGCCTGATGC TATAANTGAN TGAATTACAT 50
GNTCATTNGT TAAATTTTGT TCTAAACCCA TTAGGAAATT GT 92

(2) INFORMATION FOR SEQ ID :113:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :113:

25 GATTGTTTTT GCATTGCGTG TGTACACAG CAGCACAAAG ACAATATATG 50
TAAGCGTNNA TACACCAGAT TTGACACAAG AGATAGCGAA CACCACAAAG 100
ATTAGGACAG ACCGCGTATA GTAGCTCTGA GGAAGTCCAA GAATCTAGAG 150
30 GG 152

(2) INFORMATION FOR SEQ ID :114:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

76

(xi) SEQUENCE DESCRIPTION: SEQ ID :114:

50
TTGGCACTGA CATCCAGGAC AACAAATGCA GCTGGCTGGT GGTTCAGTG
100
5 TCTGCAACGG GCCACTCCAG AACAGTACCA ATCCTGAAGG AAAATACNTG
150
GCAGAAGGAG GCTGAGAAAG TGGCTCCGTG AAGGCNCTAT AGAGGGCTGA
182
10 TCTGCCAGCA TGTCTTCAAT ATGAGGAAGG CA

(2) INFORMATION FOR SEQ ID :115:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :115:

50
GGCACTGACA TCCAGGACAA CAAATGCAGC TGGCTGGTGG TTTCAGTGTC
100
25 TGCAACGGGC CACTCCAGAA CAGTACCAAT CCTGAAGGAA AATACNTGGC
150
AGAAGGAGGC TGAGAAAGTG GCTCCGTGAA GGCNCTATAG AGGGCTGATC
182
30 TGCCAGCATG TCTTCAATAT GAGGAAGGCA NT

(2) INFORMATION FOR SEQ ID :116:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :116:

77

50
100
150
200
227

GAGGTTCTTG AATATGTATT TTTTACTGAA AAAATCATTG ATAAANTAAC
ATACAAAAAT GTACAAACAC ATGAGTAAAT AATGTAATGA CAAAGGACTA
TTTTCGGAAA AGTGTTTTTT AAAACANNCT AGATTTCAGT GCAAAAATGT
ACCCCTGGCA CCTCTTAAAA CGTAAGAGCA AGCTCAAAAA CACGTAGTGA
TGGAAATAAG CTAGCTACGC TCAATGC

10

(2) INFORMATION FOR SEQ ID :117:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :117:

50
100
150
172

CGAGAGATTG GTAATGAGGA AGCAATTGG AGGGGNGGAA GCTACAANGA
NNNNGGGAAT TACAACAATC AGTCTTCAA TTTTGGACCC ATGAAGGGAG
GAAATTTTGG AGGCAGAAGC TCTGGCCCCT ATGGCGGTGG AGGCCAATAC
TTGCAAAACC ACGAAACCAG GT

30

(2) INFORMATION FOR SEQ ID :118:

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :118:

78

AATGATGGAA GCAATTTTGG AGGTGGTGGA AGCTACAATG ATTTTGGAAT 50
 TACAACAATA GTCTTCAAAT NNGGACCCAT GAAGGGAGGA AATTTTGGAG 100
 5 GCAGAAGCTC TGCCCCTATG NCGTGGAGGC CAATACTTTG CAAAACCACG 150
 AAACCAAGGT GGCTATGGCG GTTCCAGCAG CAGCAGTAGC TATGGCAGTG 200
 GCAGAAGATT 210

10

(2) INFORMATION FOR SEQ ID :119:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :119:

GGTAAACACA AAGAGTTTCT GATAGTGTCT GCACAACAGC AAACCAACAT 50
 25 TTGGTGAGGA ATTAGCAATT TCTTGCCAAA GAAAATTGAT TCTGC 95

(2) INFORMATION FOR SEQ ID :120:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :120:

GGAGTATTTN AANNTTCAA ACTTTATTAC TTAATGAAAC AGTTTCTATA 50
 40 TACTGCTTCC AATATACTTT AATCCTTTTT TTCTCGTTAA ATTTTTTTTG 100

79

TTGTTCTTCA GTTGAGCTGA GATACTTTTA ATTACTTTTT ATTAAGTGCT 150
TCCAGAAACC GTAACAGG 168

5 (2) INFORMATION FOR SEQ ID :121:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :121:

GGAGTATTTA TCTTTCAAAC TCCNTACTNA GTGAAACAGT TTCTATACCA 50
CTGCTTCCAA TTACTANCTN TTTNTCNGT TAAATTTTCN NCTGTTTTTC 100
20 AGTTGAGCTG AGATACTTTT AATATNNNGT NACTGCTTCC AGAAACCGTA 150
ACAGGTGCAG GAATAATTGA TGATATCCAA GTAGAGGCTG ATGNCAGCTA 200
25 ATACATACTT CGGTGACNTT ATGCATCATG A 231

(2) INFORMATION FOR SEQ ID :122:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :122:

TCTATGGCAT GAATGTTTGC AACCAACNNN NNGGAAAGCC TTAAAGGAAT 50
40 AGCTGTTTAC ATAGGAGACC GTGACAATGC TGTACGCAAT GCTGCACTAG 100

80

ACACCATTGT ACGGTGTACA ATGTCATGGG ATCAGGTGTT CAACTGATT

150

GGAATCTTTC TGAAAAGGAT ATGA

174

5 (2) INFORMATION FOR SEQ ID :123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :123:

CTNNACAGGA GAAGNAAGTA ATGATCATTC CCCAAAATG TTCTGTTATC

50

AACTGNNTTT ATAAAAATC GATTGTGGGT AGAAGCAGAG AAAAGGCACT

100

20

TAGTAAAGAT ACTACATGAN GAAAAANNTC TGCCCTTTGA ATTCTTANGA

150

AACATNNTNG NNGAATCAAT

170

25 (2) INFORMATION FOR SEQ ID :124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :124:

AAGTAATGAT CATTCCCCAA AAATGTTCTG TTATCAACTG NNTTTATAAA

50

AAATCGATTG TGGGTAGAAG CAGAGAAAAG GCACTTAGTA AAGATACTAC

100

40

ATGANGAAAA ANNTCTGCC TTTGAATTCT TANGAAACAT NNTNGNNGAA

150

81

TCAATNT

157

(2) INFORMATION FOR SEQ ID :125:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :125:

15 CAACTTGAAA TACATTATGA TGTCTGATAT GATTAAATAT CATTGAGNAT 50
CTTGCAAACA AAAAAAGCAA AAAATTAAAT CTCCATATCA ATCTTAAATT 100
CTTGGCATAT TTACTTCTGG TAAATATTAC TTCTGGTCCT TATTCTATAT 150
20 GTGTTATTGA AATTGTGTT 169

(2) INFORMATION FOR SEQ ID :126:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :126:

35 GTTTNGTTNN NNNNTGTTCC ACCTTTTGTT GAATTTTAGT TGTTAGGCTG 50
AACCTCCGAG CAGTTTNAGG ACTTGCCTGA GTTTTCTTC 90

(2) INFORMATION FOR SEQ ID :127:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs

82

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :127:

TTTAGTTTAC TTCTGTTCCA CCTTTTATTG AAATATTAGT TGTTAGGCTG 50
10 AAAGCCTCCA GTTAAGAACT TGCTGAGTTT TTTGTTTCAG CAACTTGACA 100
TTTACTATGC GCATTATATA NCTCAATTAT GTCTGTTTTT TATGCTAAGT 150
15 AGGAAAACCA 160

(2) INFORMATION FOR SEQ ID :128:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :128:

30 GCCCACAAC TACATCCTCA TTATTGGCGC CTACAACTC AACTACGAAC 50
ACACTCACAG TCGCATCATA ATCTTTTGAG GACTTCAAAC TTA CT CGGCT 100
ACCGCTTTTT GATGACTTCT AGCAAGCCTC GCTAACCTCC CTTACCCCCC 150

35

(2) INFORMATION FOR SEQ ID :129:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :129:

5 AGAGAGACAG ACACCATGGA GCCACAGGGG CAAGAGGNNG NTTTCCGAAG 50
CAGGGGANNG GCTATCACTC GGACGGACCN NNGCTCAACG AGTCCCACGA 100
GAACACACCA GAAATTTGTC ATTGCACTCA ACCAAAATCG ATATCAGCAA 150
10 TGAAAAACCC AAAACAGTTA CGANGCTAAT CC 182

(2) INFORMATION FOR SEQ ID :130:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :130:

GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT 50
25 TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGTC 100
TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT 150
30 TCAACCAAAA TCGATATCAG CAATGTAAAA ATCCCAAAAC ATNTTACCGA 200
TGCTTACTTC AAGAAGAAG 219

(2) INFORMATION FOR SEQ ID :131:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :131:

5 AATAATTCAT CCACTTATGG AGGAGGAGGA GAATGTGGAA GAGGTAAAAA 50
GCTGGGCACA AGTTCATATG CCTATGAGTC AGTAAAGACT GAAGTAATGT 100
CCTATGTTGA GCTGGTTATT TTGATATATG ATAATAATTA TCTTTGTAGT 150
AGAACATCGT TAACGGAATC ACAGATATAT C 181

10

(2) INFORMATION FOR SEQ ID :132:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :132:

GACCAGCAGC TGTGGACATT ATGAGAAAGT GAAACCTGAG ATCCNCTGTT 50
25 GATTGAGAAA TGCAACACCT CAAAATGNGG GACAGCTCCT GATTACCAGG 100
TAGAAGATGN AAACAACTGG GGTGTCCATT CAGGAGGAAA CAATTGCAAG 150
CTAAGAACTG TTGAGAGTGA AGCTGCATTT TCTGNACC 188

30

(2) INFORMATION FOR SEQ ID :133:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 190 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :133:

85

GAGGTTGGGT CGTTGCATCC ATCATCAGGA GTTGACTTGT TCTGAGCAAC 50
TGAACAGAAC ACACCGCGAT GCTCTCGACA CTCCGCTCCT GGACTTCAGT 100
5 CACGAGTGAG TTGATGGTGA CTTGACCTGA GAGATTTAC AGAAGCTCTG 150
TGAAGTGGTT GTGGAAGAAA TCTGAACTGT TCAAGTTAAC 190

(2) INFORMATION FOR SEQ ID :134:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :134:

20

ACATTACGAT CACTGATAGT TGGTGTGCGA CTGAAACCCA CATTNTGGTC 50
AATCTCCTCG TAGAGCTTCT TCTTCACCTG AGGATTGGCA GCAGGAAGGC 100
25 CAGGGTCCAT TTAAC TAAGA GGTGGTGATC TCCACGCCAG CCCC AAGAT 150
GTCCCTATA TGGTGAGAAT GNGTCATCTG AAAGCAGCTC TGAGTCTTGA 200
TCTGGGCCAG CATTGCCATT ATTGAGTTTA TCTAG 235

30

(2) INFORMATION FOR SEQ ID :135:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :135:

GAGAAACAGT ACCATCCANG ACACGATGTG GTGGAGGTTG ACNCCGCTGT 50
 ACCCCAGAGG AGCNCCACCT GTCCAAGATG CAGCAGAACA CTACAAAATC 100
 AACTATGTTT TTTAGCAGAT GCAGGACTAG ACCCCCACGC AGCTCTG 147

(2) INFORMATION FOR SEQ ID :136:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :136:

GAAAAATGNG TTGANCCATT CATCCACAAA TTGACTTGCC TGAACAACCA 50
 CCAAACAATA CACTAATGNT TCACACNTTT NCTTTTACTT GNACNTTAAG 100
 NTCCCANTGA GTCACGGTGA CTTACCCTAA ACATCTCAAN NGTNNTCTGA 150
 CTNAGAATGC GGAGGAGATC T 171

(2) INFORMATION FOR SEQ ID :137:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :137:

ACATATATGT GGTAGGATAG AGAGATGGNN NNGTGTATG ACATAGGTGT 50
 TTCTCGTGTG ATGAGGGTTT ATGTGTTATG TGGGGTGAGT GAGCCCATTG 100

87

TGTTGTGGTA ATATGTGAGG AGTATAGGCT GTGACTAGTA TGTGAGTCT 150
GTAAGTAGG 159

5 (2) INFORMATION FOR SEQ ID :138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :138:

CCCACGACTT ACATCCTATN ACNCTTCGCC TAGCAAATA AACTACGAC 50
NCACTCACAA TCGCTCATAA TCTCTNAGG ACTTCAAAT NTCTCTNTGA 100
20 NCCTTTTGAT GACTTCTACA AGCCTCGCTA CCTCGCCTTA CCCNTGTNC 150
TNCGGGAGAA CTCTCTGTGC TGTACCAGT 179

25 (2) INFORMATION FOR SEQ ID :139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :139:

GACCTGGGAC GTAAATGATG AGACGGGTAC TTTGGCGGAC ATGAAGGAAC 50
TGGCATATGG AACCTTGGCT GTGAAGCTGC AGACTATAAG ACAGCATGAG 100
40 ACGACAATTC TGCTACTGCA ATGATGACAT CGTTTCAGAC CACAAAAAGA 150

88

AAGGCGATGA CCAGAGCCGC AAGGCNG

177

(2) INFORMATION FOR SEQ ID :140:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :140:

15 GTTTACAACA TTTACATCCT ATGAATCAT GGATTATAAA ACATTTGTGA 50
CTTATACTGT CTNTGTCAGT TA 72

(2) INFORMATION FOR SEQ ID :141:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :141:

30

GTNGGCTGAA ATGAAANAAT AAAACCAAGA AACGAATTGA AGTATTNGTT 50
TTAGTACGNA AA 62

35

(2) INFORMATION FOR SEQ ID :142:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :142:

5 ACCAGTNNNT GATTGGTAAA TGGGAAATAT AATTGATTCT GATCACTCTT 50
GGTCAGCTTC TCTTTCTTTA TCTTTCTTTC TCCTTTTTTA AGAAAACGAG 100
TTAAGTTTAA CAGTTTGTCA TTACAGG 127

10 (2) INFORMATION FOR SEQ ID :143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :143:

AATATAAAAG ACAGCAGTTT CACATTTTAC ATATTTGAAA AACATTTCAA 50
AACCCTCTAA TAAGTATTTA ATGAAAATAA ATTTATCGAA GAGAAACAAT 100
25 GACCACAAAA TTAATACTAC CAAATCATTG CTGAGACTTT TTGCATTACA 150
ATATTTGGAG AGTAGGTGAA GAAAATATAG AACAGAACAT GNACATT 198

30 (2) INFORMATION FOR SEQ ID :144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :144:

GTTTCTCTNT ACGTCATCCA CCTTGACATG ATGGGTCAGA AACAAATGGA 50

90

AATCCAGAGN CAAGTCCTCC AGGGTTGCAC CAGGGNNTAC CTAAAGCTTG 100
TTGCCTTTTC TTGTGCTGTT TATGCGTGTA GAGCACTCAA GAAAGTTCTG 150
5 AACTGCTTT GTATCTGCTT TGNA 174

(2) INFORMATION FOR SEQ ID :145:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :145:

GAGAAATAGT ACTTTAAAAT AAAACTAACA TGGTTTGATC AGCTTGAAAT 50
20 AAGATTCATA AAATGTACCT TTTTGTATTG TTTTGTCTN GAGTTTTCGA 100
TTGAGANCAT TTGGTAAAGA TAAAGAGGTT TCCTGGGTGG CAAAAAATTA 150
25 TTTTGG 156

(2) INFORMATION FOR SEQ ID :146:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :146:

AAGATTCNNN NNTCCATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG 50
40 GTTGGAATT GGCTGTTTTG TTAAATATA TCTTTTAGTG TGCTTTAAG 100

91

TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTAAT 150

T 151

5 (2) INFORMATION FOR SEQ ID :147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :147:

CTTTATTTTT CTTATACAGA TTCAGAGAAG TAAAANNCAG TACCAAATC 50

CAGGTAANNT GGTTCGATCT GATCGATTG GCTGCATACT TTCGGTACGT 100

20 ATAAACATTCT AAACCTAAAA TAGAAATTTT TATATTACAA AACGAGGAAG 150

TAAAATTTTA AAAGTTAAAG TACTAGC 177

25 (2) INFORMATION FOR SEQ ID :148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :148:

GATTCNNNNN TCCATTGAAT GTTACCTGTG CCAGAATTAG AAAAGGGGGT 50

TGGAATTTGG CTGTTTTGTT AAAATATATC TTTTAGTGTG CTTTAAAGTA 100

40 GATAGTATAC TTTACATTTA TAAAAAAAT CAAATTTTGT TCTTTAAT 148

92

(2) INFORMATION FOR SEQ ID :149:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :149:

AGATTCNNNN NTGGNATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG 50
15 GTTGGAATT GGCTGTTTTG TTAAATATA TCTTTTAGTG TGCTTTAAG 100
TAGATAGTAT ACTTTACATT TATAAAAAA ATCAAATTTT GTTCTTTATT 150
TTGTGTGTGC CTGTGATGTT TTTCTAGAGT GAATTATAGT ATTGACGTGA 200
20 ATCC 204

(2) INFORMATION FOR SEQ ID :150:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :150:

35 AACATCGAGG TCGTAAACCC TATTGTTGAT ATGGATCTCT ATGAATAGGA 50
TTGCGCTGTT ATCTCTAGGG AACCTCACCG TTGGCAAGTT ATT 93

(2) INFORMATION FOR SEQ ID :151:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

93

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :151:

AATCGAGAGA AAAAATGATG ACACTGTAGC AATATCGTCG GANTCCACCT 50
10 ACTTTGGGAT CAGCCTATCC ATCCGTGTCT TCCTATTAA ATCGTCTATC 100
CTCTATCCTT CCCCTGTCTT TTTNTGAAAA GGAAAAAAC CAGGAAGGTG 150
15 T 151

(2) INFORMATION FOR SEQ ID :152:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :152:

TCTGAGAGGA ATACTNNTAA GTGCAATGAA TATTGCAAAT TTTCCCCCCT 50
30 CTAAGTAATT CCCGATATTA GCAAANCANN NANATTAATG TCCCAGTGAA 100
TGTAGCCTC 109

35

(2) INFORMATION FOR SEQ ID :153:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :153:

5 AAAATTATTT TCACAGTCCC CCCCAACTCT CATTGCGTCG TTAAAGTCCC 50
TCCAATCCTT TTTTAGTTGT GAAAAAATAA GGGGCCTTTA AAGGAGGAGG 100
AGGAAAAGGG GAAAAAACC CATAATGGGC CTAAAA 136

10 (2) INFORMATION FOR SEQ ID :154:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :154:

CATCTTCATC ACCATCACAA TACTCATCAT CACCACCCTT CATNCACTAT 50
CATCTTCTAT GACTGCAAAC TTCTTATCTT TCTCTTCATT ATAGAAAGTT 100
25 TCAAGATGAG TATACGCATC TATCATTGCA ATTGTGTCAT TAATTGTAG 150
GGCCTCATTG 160

30 (2) INFORMATION FOR SEQ ID :155:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :155:

ACCAGTNNNN NNNGGTCAAA TAGGGAAATA TAATTCGATC TCTCGAATCA 50

95

ACTCTCTGGG TCAGCTTTCT NCTTNTCTTC TATCTTTNCT TNTCTCCTTT 100
TTTAAAGAAA AACGAGTTAA GTCTTAACAG TTCTCGCATT ACAGGCTTGT 150
5 GACTTCATGC TTAGTGTAAG GTGGAAGTTG AGATATTTTA A 191

(2) INFORMATION FOR SEQ ID :156:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :156:

CAACTGAACG CTTTGCTCAG GCTGCTACAA TGGAAGGAAT TGNGGGCNAN 50
20 TTGGTGGAAC TCCTCCTGCN NTCAACCGTG CAGCTCCTGG AGCTGAATTT 100
GCCCCAAACA AACGTCGCCG ATACTAATAA GTTGCACTG 139

25 (2) INFORMATION FOR SEQ ID :157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :157:

GGTACAGAGC ACTCTGTACC AACACACAGA ATTTACTGTT CTGCAAATGA 50
CCAATACTAA AAATTTATAA AGATGTGCAC AATTNNNNGC AGGCAATCTT 100
40 TCTTTTGTTT ACAAGATACA ACATTTAACA GTTATTAAAT GTAATCCTGA 150

96

AGCACCCGCA AATTACCTT TG

172

(2) INFORMATION FOR SEQ ID :158:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 10

(xi) SEQUENCE DESCRIPTION: SEQ ID :158:

15 GGGTGGCTGT TNNGTATATC TCGTTAGTAA ATGTACATGC TCTTCAGGTT 50
CTAGGGCTCC TGTTAGGGGA GGGAGAAATG TTGGAAGNGG GGG 93

(2) INFORMATION FOR SEQ ID :159:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 25

(xi) SEQUENCE DESCRIPTION: SEQ ID :159:

30 GNATTTTTTT ATTGATATAT CATAGTTGTA CAAACATTG GGAGTNCANG 50
TNGATACTTT GATACTATCG TGTNNNNNGG ATAATCACCA AATTGGATTC 100
35 CA 102

(2) INFORMATION FOR SEQ ID :160:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

97

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :160:

GCTTTTNNNN NNNNNNNNNC AGGTTTATAT TTACAATAAT TATCTTCCTA 50
TAGAAGCAAT AANN CNAGTA TTCTCCAGTA ACAACACANN NNNATATTCT 100
10 ACTCATCAGA GTTGGGAAAA ATAGGAATAA AGCAGATTCC ATACAGAAAT 150
ACCGTACTCT GCATATGTAC AAATAAATTC AATATATTAA ATCATTTTGA 200
15 GCGGA 205

(2) INFORMATION FOR SEQ ID :161:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :161:

AACTTTTTTA ATGGGTCTCA AAATCTCTGA GACAAAATTA CTNNGNNNAA 50
30 AGTTGTTTTC CATATAAAAA ANNNNNNTGA TTTTAAAAA ACTAANNAAC 100
TTAAAAACNT GCCACACGCA AAAAAAGAAA CCAAAAGTGG GNCACCAAAA 150

35 (2) INFORMATION FOR SEQ ID :162:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :162:

5 TATTCAAAG AAAACATGG GTAAAAATGA TAGTGTTAA TCTGGCTCT 50
GTGTACATAG ATAGATACCT GTTACAG 77

(2) INFORMATION FOR SEQ ID :163:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :163:

20 GAAAATTATT TTCACATCCC CCCCAACTTC TTGCTCTTAA TCCTCATCTT 50
TTAGTTGAAG AATAAGGCTT AAGAGAGAGA AAGGAAAAAC CATAATGGCT 100
AACTTAGCAG CACAACACGG TTCTTTTATC AAGGCGTNAT CATCATTTCT 150
25 CAAACTGACA TGCTACAGAA ATGTCTTCCA AA 182

(2) INFORMATION FOR SEQ ID :164:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :164:

40 GAGGGAGCAA AGAGAGCCAT AAAGGCTCGT GCTGGGAAAG AAAGCTGTTA 50
TGCTTAGACT TCTCTAGGTG AACTCAGAGT CTTCAAGAG GAAATGTTAC 100

AAATTGTCAC CCGCCAGCTT TCTGGCCAGT AAGCAGAATG CCAGGTTGCT 150

CAGATTCACA GACATTTGCA AAACAGAAGA TG 182

5 (2) INFORMATION FOR SEQ ID :165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :165:

GTATCTCCCT CTACATCCCT CCCGAAATAC TAGGAATACT TATTCTATAT 50

GAGACATATA TACCACCCAA GTTTAACAC CATATCCCAT CGGCTGTTAG 100

20 TGTATATAAA AAGAAATAA 119

(2) INFORMATION FOR SEQ ID :166:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :166:

35 GTACAAAGCC ACTCATCCTC GTGTGCCTAT CACGTTTTC AAACACATAG 50

GATCCCATCT CAGGAGCAGG ACCAGTGTTT AGCTAGATTA AACTTCGCTG 100

GTGATCTTGT TGATGCATAT AAAGTAATCT GGCATATATG GTTAAATTCA 150

40 AGATGTTATG GCAGAAGTGA CTTGTTTTGC TCAACAAGCA TTG 193

100

(2) INFORMATION FOR SEQ ID :167:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :167:

GTTCTGACTN AGAACTGAGC ACATAGCATT GACGCGGTAC CCTTGGAGAG 50
GGTGTGCTAG GAGGAGTGCT TGGCGAATTT GGACACGTAC TAATGTCTCT 100
GAGCCAGTCT GAATCTCTGT GAAGATGCCC CAGTGGAGGT GGCTGAAGAT 150
TAAATGGACA GTTTATAAAG TGTCTCTGGA GCCGA 185

20

(2) INFORMATION FOR SEQ ID :168:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :168:

GGACAACACA GCACCCATCC ACTACCCATT CAGAATTTAT ATAGAATATG 50
TACCCATGAT TATCTAGGTG AATCAATGCA ACAGTAGCTC TGATGTCCAG 100
ATTTCCCTAGT CTATTATTTT GTGTACAGAT CCTCTAACCA CTTAGAAATA 150
ATTTTAAAA ATA 163

40

(2) INFORMATION FOR SEQ ID :169:

101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :169:

10

AGACAAATTC NNNNTNNNN NTGCCTGATA ATTCAGATG CCACCGTATA 50
GCAAAGGGTG AACATGTTTT CAACCCTTTA ACTTTTACG GTGTTTGAAG 100
ACCAGCTACT CCTTAATATT TATCAATGGA TTAAGAAGTT TAAGATTTTG 150
CAGATTACA ATTTGGGTTT TTGTCTGGAG TTGCTTCGGT TTGAAGCCCC 200
CT 202

20

(2) INFORMATION FOR SEQ ID :170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :170:

TCAGGGAACC AAAAACTGG CTTGCTTGGC ACCCAGGGAC ACTAGCTGTT 50
TGGCTCTCCA CCCAATTAAA AAAACAAATC CCTGCCCTTT CCCCCACCCC 100
ACTAGCTAAG CAAGAGCAGA GCTCTGATGA AGAGCCAGTG CCGGGTGCCT 150
GGTGCCCAGG GCTGTAAA 168

40

(2) INFORMATION FOR SEQ ID :171:

102

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :171:

10

AGAAGTCAAC TAAAGCTTCA ATGCATCAAT TTATAANGCC TCANAGATCA

50

GCAATTTATG ACACTTACAT TTACAGTCGA CCTTTACTAA CCAGGCAAAC

100

15

TTCCCGAAAT GATCAGGACT GATTCATCTC CTGAAATTNN CNGT

144

(2) INFORMATION FOR SEQ ID :172:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :172:

ACCCACAGNN NNNACCTAGA GGCCACGCGC CCAGAGAGGC ACGTAGAAAT

50

30

GGGGACAGCA CGTTTATAGA CCACCAGAAA TTGAAGAGGA A

91

(2) INFORMATION FOR SEQ ID :173:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

40

103

(xi) SEQUENCE DESCRIPTION: SEQ ID :173:

5 GATTTTTTAA TGGGTNGCCT CTTTtagCTT GGAATATTAC GTTACTTTA 50
 ATCCAAGTCT AGGCCTTTTA AAGGGTCCTT AAAATTAAAG TTCAGAATGT 100
 GAATCCCTTT GACATCTATT ACAGGTTATA GGACCTTTTT GGTGTGATTA 150
 CGGTTTCAA TACGATTGTA TAAATGAAGT TAACTTGGCA GAAGTTAAAA 200
 10 TGGA 204

(2) INFORMATION FOR SEQ ID :174:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :174:

25 GTAAATTCA CTACATCTTT TNNNTGACT TTCATGCATT TCTCATACAT 50
 TNNTNNGA TGCTTGACTT TATTGCTTCC TAGCAATAAT CTGCATTAA 100
 ACGAAAGGCG GTTCAATTCA TCAACTGAA ATGACTATTT ATTTTNNAGG 150
 30 ATTTTTTAGG GGAAGAGTAC CCATTTCGTT TATAAAAACA GATGACAAAT 200
 TTCTTAAAGA AACAGAAGCA CAATACTTTC GAAATACAAC G 241

35

(2) INFORMATION FOR SEQ ID :175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :175:

5 GGTGGGCTCN NNNANNANNG TTCTACACTG TGGTATAAAC TTGTCGTGGT 50
TCTCGTGATA GAAAACAGAC ACTGACCTTG GGTATAGTGG GCCTATAAAT 100
AACAAACCCT TGGGTACTCC TGAATAGGGG CAGGGCCCCC TGGGCCTCCC 150
10 TTACAGGTTT CTTCAGGGAA ATGGTCCCTG GGATAATTCT TTAGGGCCCT 200
TTGGCCCTTT T 211

(2) INFORMATION FOR SEQ ID :176:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :176:

25 AAAATAAGAA TAAACATCCA TAATAGTNAT AGATANATCC NTTTATTTAG 50
NACATCAGCA ACGACTGCTT CACACCAAAT CCCTTCCTCT GNGAATGATN 100
30 TATATAACTC TAGTACTGCT TTCCATGAAG AACCTTGCAA ATTGATTGAA 150
AGTCCAGGAT NNCTCGCTAA TCCTCCACCA TAAGATTTCT GACCTATGAT 200
AACTCCAAGG TGGCAAACAG AGAAATCAAC TTCCTTATAA ANAAATCCNA 250
35 AT 252

(2) INFORMATION FOR SEQ ID :177:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid

105

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :177:

GCGGGCGACT TTCCATCCCT CGAACCAAGG CATGTTAGCA CTTGNCTCCA 50
GCATGTTGTC ACCATTCCAA CCAGAAATAG CACAAATGCT ACTGCGCGAG 100
TTGCAGCCAA TCTTCTCAA GCAAACCGAC TTCCTAACAA CTNTCTACAT 150
CTGGCTCGCT GCAGGCGACT CAATGAAATC CATCTTTAAC ACCACAATCA 200
TTGTTTNACA CCCAGTGTGC AAGCCAGGAG GGCATGTTCT GAGTCTNTCC 250
ATCTGAAGAT ACCAGCTTCA AATACTAAT 279

20

(2) INFORMATION FOR SEQ ID :178:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :178:

TATGCCCTGA AATGAAACCT CTAAGTTTGA CAAAATACCC AAAAAACAG 50
ACCTTCCTNG TTAACACTTT ATAAGAAGGT GTGACATTG GTGGGTGGTC 100
GTTCTCAATT TATAAANA TAAATGACTT TAAAGGAGAA ATAAATTTAT 150
GTCAGGA 157

40

(2) INFORMATION FOR SEQ ID :179:

- (i) SEQUENCE CHARACTERISTICS:

106

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :179:

10 GATAATGCAA CTTTGTGACAG GAAAGCGCGA TTTTACTAT 39

(2) INFORMATION FOR SEQ ID :180:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :180:

GCAAACTCAA ACTACGGACG CACTCACAAT CGCTCATAAT CCTCTCTAAG 50

25 GACTTAACT CTACTACACT AATACTTTTT GATGACTTCT AACAAAGCCTC 100

GCTAACCTCC CTTACCCCCC ACTATTAACA CGGGAGAACT CTCTGTCTAG 150

30 TACCACA 157

(2) INFORMATION FOR SEQ ID :181:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :181:

107

CCATCCAGGC CAAATAAGCN CCGGCTATGC CCNTGTATTG GATTGCCACA 50
CGNCTCACAT TGCATGCAAT TTGCTGAGCT GAAGGAAAAG ATTGATCNCC 100
5 ATTCTGGTAA AACTGGAAG ATGACCCTAA ATTTGAAGT TGATGATGTG 150
CCATGTGATA TGGTTCTGAC AAACCCATGT GCGTTGAGAG CTTTT 195

(2) INFORMATION FOR SEQ ID :182:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :182:

20

CATGGTCTTA ACCAGTGTCA GATGGAATCA GTGGATAAAT CCCCAGGTTT 50

GTTTGTCTT CAAATGGGAC AATTGAGGA ATGCTTTAGG CAGAGGACTC 100

25

AGATGACAGA GCGCCAACCA CCCACAATAG AACCTGCTC ATCACA 146

(2) INFORMATION FOR SEQ ID :183:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :183:

TAGAGGAATA GGGNNNGNGA CGCCCNAGT TGTAGGGACG GACGGAGGAC 50

40

(2) INFORMATION FOR SEQ ID :184:

108

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :184:

10

ACGNTTACGG TCACTGATAG TTGATGTGCN NCTGAAACCC ACATCCGATC 50
AATCTCCTCA TAGAGCTTCT TCTTCACCTG AGGATTGCGC AACAGGAAGG 100
CCAGGATCCA TTTACCACAG AGGCGGGATC TCCACGCCAA CCCCAAAGAT 150
GTCCCCTATG ACGACGAGAA TGTGATTATC TGAAAGCAAC TTGATCTTGA 200
TCTGGGCCAG CATGCCTCAT CTGATTCATC TCGCTTCCAT CAATGNGT 248

20

(2) INFORMATION FOR SEQ ID :185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :185:

AATGATGAGT AAAAGATTCA ACAACTCACA GCCCTGGGGG CACTCAGGCT 50
ACTGCTAAGG CCTGAGAGTT TTGCAAAAAT GCGCAGAGAA ACACCCTTTG 100
AACGTGGCTT TCT 113

35

(2) INFORMATION FOR SEQ ID :186:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 148 base pairs

109

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :186:

GGGCCCCCTG ATCAATTCTT TGGATGCTTT TCAAATTTCC CAGGATCCCG 50
ATGTCGTCAT ACACTCCGAA CATGACCCTT TTTTCTTCCA ACGATCAACC 100
ACTNCGNGGG ACGGGAGAGT GAGCCTTATA CCGATCAATC TGCACACC 148

15

(2) INFORMATION FOR SEQ ID :187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :187:

TCCTTACTGT AAGAGCCATT TAAACGATTA AAATCCCACT NGCCATACCG 50
TAAGATGATA GGACCAACCA TACCTACCGA TCAAAAATTT ATCAATCCAA 100
GCCAACTACA CTCCCACTGC TAAAAAGATG AAAGGACCAA TCAAAGATTT 150
AATTAACTA AAGGGAAAGA ATCAGAGACA GAGAATGAAG AAAGAAATTC 200
TAAGTTGCGA CCGACAAACC AGAACAGACA ATGAAGCCTT TCAACTGC 248

35

(2) INFORMATION FOR SEQ ID :188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

40

110

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :188:

TATGAAGAAG TGCAGCACTG GCCAACACCA GGGTTTACTG AATCATTCA 50
GTTTAATACA TAAGTGCCA ATAATAATGT CAACCCTCCC TCGCCACAGC 100
CAATAATTG TCCTCACTGA GTTGGCAACA AGTGACTGCT GTGACT 146

(2) INFORMATION FOR SEQ ID :189:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :189:

25 ATTTACCACA AGGGACGATT TCCACACCAA CCCCAAAAAT GTCCCCTATG 50
ACGACGAAAT GTGTATTTGA AACAGCTCTG A 81

(2) INFORMATION FOR SEQ ID :190:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :190:

40

AAGTACAGCA TCCTGCTGCA AAAATGATTG TAATGNCTTC TCATATGCAA 50

111

GAGCAAGAAT TGAAGATGCA CAAACTTCGT TCTGAATTG TGAGCTTCCT 100
GGATCAACTG AAGAACTTCT GAGGATTGAC CTGTCA 136

5 (2) INFORMATION FOR SEQ ID :191:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :191:

AGGATTTAAG ATGGGGACAG ACTGGTGAAA ATGCGGCTGA CTGGAAGGAA 50
ATGGGGCATA CGAGTAATAT GTACATATCA AACAATCAAT TGCCTCCTGA 100
20 AATCAAAAAA TCAAATGGTG AAATGGAGCC TCCTTGATAG TTTAGGCCAA 150
CA 152

25 (2) INFORMATION FOR SEQ ID :192:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :192:

TAAGCGAGGN NGTCTTTGAT TGCCTAGTAA GGTAAAGACG ATTTTATAGA 50
ATNAAGGTGA TTCCT 65

40

(2) INFORMATION FOR SEQ ID :193:

112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :193:

10

AGGACCCAAA CTACCTTATT GCATTGAAG TTTTACTTAT NCTATTATAA 50

TCTAAGAGCC CACCCAACAA GGCACTACAC ATAGATGCTC ACACTCTATA 100

15

GGCTGCCTGA TCCTGGACCA CCTGGGGCCC TGATTATGAT CTCCACGGGG 150

CTGTCAATGA CTAGGGAAAG CTTTTTAAGA CCCAGCGATC ATGCAATGGC 200

TCAACCATGG CGAATCAAAG TTAGCATAAT GTCCCAGCAA ACAATGTTA 249

20

(2) INFORMATION FOR SEQ ID :194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :194:

GGAAAGGGTG CCTCATCCCA GCAACCTATC CTTGTGGGNG ATGATCACTG 50

35

TGCTGCTTGC NNCTCATGGC AGAGCATTCA TGCCACGATT TAGGTGAATC 100

GCTGCATATG TGA CTGT CAT GAGATCCTAC TAGATGATCC TGACTAGAAT 150

GATAATTAAA AGTATTACT TCGAAGCACC ATTGAATGN TCAT 194

40

(2) INFORMATION FOR SEQ ID :195:

113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :195:

10

GTGATTTTAG TTTAAGGATA AGAAGCCACT ATATCAACGT CGGGGGGGTA 50
TTTAAGTCAC ACACATAGTT AACAAACNCNC GTNGCGTGCA ATAAATACCA 100
CATCCTTTNA TATGNNCNGN A 121

15

(2) INFORMATION FOR SEQ ID :196:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :196:

30

GGGCTTCNNN NNNNNNCATG TGCACCTAGA ACCGTTACTA ACCGAAACAC 50
CATTTGCTTG TCAACAATGT ACCCTTGACA GCAGGGAGAA ACTTCTTTAT 100
AGTCTCTGCT TCAGACAAGA TTTACNGCTT TCTCCAAGGC CAGAGGCAAA 150
TTGTGACCAC AAGTCTTGTT TCTTG 175

35

(2) INFORMATION FOR SEQ ID :197:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

114

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :197:

5
ACTGGCAACT TCTATGTACC TGCAGAACCC AAATTGACAT TTGTCATCAG 50
AATCAGAGGT ATCAATGAAA TGAGCCCCAA GGTTCGAAAG CTCGCAACTT 100
10 CTCACCTTC ATCAAATCTT CAACGACCTT CGCAACTCAA CAAGCTTCTT 150
ACAGTGAGGA TTGCAGAGCC TATATAGCTG ATACCCCAAT CTGAATCATA 200
15 AATGACTAAT CTACAAGCNT GTTATGCAA ATAAATAAGA AACGACTTGC 250
TTACAGATGC NTTTTAATTG TGG 273

(2) INFORMATION FOR SEQ ID :198:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :198:

30

GATTCCCCAA TAAGCAGACA CCTTGAACCA GCCTGGGGTG AGCGAAAGAT 50
GNTATA 56

(2) INFORMATION FOR SEQ ID :199:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

115

(xi) SEQUENCE DESCRIPTION: SEQ ID :199:

5 GGACGCTGNN NNNNNNATCC TGCAATGCAC AGCACAGACC CCACCACAGG 50
 GGTTTTATCC AGCCCAAATG TCAACAGTGT CAAGTTTAAG CAACTCTTAC 100
 CGAGTGGGAC TCAATTCCCN AGTTGTATGG AA 132

(2) INFORMATION FOR SEQ ID :200:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 284 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :200:

20 AAACCTTTTN GCACTTACAC AGACGAGACT TCACTGCNTG AGGATCATAC 50
 GACATTTCAA TCGNACACAA ANTAAAAAA TAAACAAAT TTTAAAAAAC 100
 25 CATNTTGAAT TTCCTTAAAA TTATTCCAAT ACTTTCCAAC TTAAATTCA 150
 GAACAAATCC TCCTAGAGAC TATCAATACC AATATCTTCA CATTGCTCAG 200
 30 CTGNTACATA CGNCCCACCA GTTCACAACT AATGACACAA CACTACATGN 250
 TCAAATCTTA TCTNNNATAG CACAGTAACA AAGT 284

(2) INFORMATION FOR SEQ ID :201:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

116

(xi) SEQUENCE DESCRIPTION: SEQ ID :201:

CCTGACACCA ATTTGCCCCA CATGTATGCG GGAAGAGGCC TGAGACTAGA 50
 5 AGTCGTTGCC CTGTCCATCT CCCGCCACA GGCTTCATTC CCAGATTNT 100
 CTTGNT 106

(2) INFORMATION FOR SEQ ID :202:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :202:

20

CTTTGGAAAA CAAACATTN TTATTACTGA AATAGCAAAA ATCATTCTAC 50
 ACTCCTCCTA AGCATGTTCA ATTAGCATA ATTCCAACAA TGCATGAAAA 100
 25 AATTNCTAGC CAGAGGCATT TAAGTGATT CTTCCTAAGT GTTGCTAAT 150
 TCAATGCCAA GAACTATGAT GTTTATCNTT CTGATGGACA AATCAAGAAA 200
 CAAAACAGAT ATAATACCAA GGGTAAAGCT GATATGACCC ACAACATTGT 250
 30 CATTACTCTA ACTGTTAATC 270

(2) INFORMATION FOR SEQ ID :203:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

117

(xi) SEQUENCE DESCRIPTION: SEQ ID :203:

5 AACTAAGGCA CATTGCCCTT TTTGACCTTT CTNNNGNACT ATTGAAATCA 50
AGCTTATTGA TTAGGTGATA TTTTATAAC AATTGAAAGG GCAATATCAA 100
ATAATGACAT ATGAGAATTT TTTATTACAT ATTAAACTG ATTTTACTT 150
TACAAAANNG NAATTGCAA TTA 173

10

(2) INFORMATION FOR SEQ ID :204:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :204:

CTGCTTCACC ATCCTGGCGT CTACCAGCCT GGTGNGGCTG GGTACTGTGN 50
25 ATCGTCTTCC TCAACAAATG CGAGACCTGC CAACCTGCAC TACACCACAT 100
CCGCNCAAGA AGAAGAACCT GCTGCTTCAT ACAACACGGG GAGGCCCTGT 150
CATTAACATT ANTT 164

30

(2) INFORMATION FOR SEQ ID :205:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :205:

118

GACCGCCCAN NNNCATCCAA AACTTCTAGG CACAATCTAT ACTGCTGCTG 50

AAGAAATTGA AGCAGTTGGG GGAAAGGCCT TGCCATTGAN TTTTGATNT 99

5 (2) INFORMATION FOR SEQ ID :206:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :206:

GTACCTTGGG NNNNNNANNG GGAATGAGGT TCTACCACTC TGGAAAATTC 50

ATGCCTGTCA NTNTAANTNC AGGTGCCAGT TNNCNNTAGG TCGCCAAAGT 100

20 TGGGGTTAGN TGTCNAA 118

(2) INFORMATION FOR SEQ ID :207:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :207:

35 CACACTANCG ACCAACACTT AAAAGNCTNC TCACACAAGN ATCTTTTAA 50

TAAAAATACC TCTTTCNTAA CTCCACTTAA ACTCCCTAAA ACCCATGTGG 100

AAGCCCCCAT CCTGGTCAAT AGTACTTGCC CAGTACTTTT AAAACTAGGC 150

40 GCTATGCATA ATACCCTCAC 170

119

(2) INFORMATION FOR SEQ ID :208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :208:

TTCAATGAAA TGCTTGATA CAATGATATA ACAAAGAAAC CCTAAGACAA 50
CGAGAACTTC AACTAAGTGC ACTCATGCAG AATCTCTGCG GGGAGAATTT 100
TTTCTCGGGG AAGTAACCCT GCCTTTGAA 129

(2) INFORMATION FOR SEQ ID :209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :209:

CTTGCGCTCA TTTTCTGTAC TTCTGACAGT GCCCTCAGAG TCTGCAGGTG 50
GATCCTTTTT TGCATGGCAT TAATTATATG AGCAGCCTCC TTCTGACAAT 100
CCAAATTTTG GCTCCAGAGT CATTTCTGAA NNTCTACACT TANGGNCTTN 150
AGCNTGCTCA TTCAAGGTNA AGGGGAGTTT TNAAAAATAT 190

(2) INFORMATION FOR SEQ ID :210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs

120

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :210:

TCATTGAGTC ATCCTTTTGT CCTGCTGCTG TAAGGTTTTT TTTCTTCTAG 50
10 TAACTGTATG ATCCAGAGCG ACCCAGCAAG GACTCAATCG ATCACCAACT 100
GATGCAGAAC TGTTTCATAT CTAGAAATG 129

15

(2) INFORMATION FOR SEQ ID :211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :211:

CTGTAAGGTT TTCCTTCTTC TAAGTAACTG TATGATCCAG AGCGACCCAG 50
CAAGGAATCA TATCGATCAC CAGCTGATGT AGAACTGGTT TCANATCTAG 100
30 AAATGGAANC NNNGNGTTT TTCCTTAATG GACCCCCCN GGGGCNGAAT 150
GG 152

35

(2) INFORMATION FOR SEQ ID :212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

121

(xi) SEQUENCE DESCRIPTION: SEQ ID :212:

5 CTTAACCCTT TGGAAGGNTT GACTGTGTGA CCCGCAGCAA ATAATTCATG 50
TCGAAAGATG AAAACAAC TA AGTTCATAAC CCCCTGCCCCG CCATTGACCT 100
CCCTTTNAAA ANCGAGACCA AGACTCCATC ACTGGTTTCG AATTTACATC 150
10 NAACTGCTAA GATTGATACA TTNCAAGTCT GCAAAT 186

(2) INFORMATION FOR SEQ ID :213:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :213:

CTTAAATGCC TGGTGTGATA TCTTCTTTAA ACCTGGAGAG ATTGAATCAA 50
25 CCTTTCTCTA AAATTCCTTT CCTTGCCTC CTCCTCTAAC TTTTCCTCCT 100
TTCNCGCTTT TCCTCAGGCT TTGNTTTTCC TCATGCTTTG CTTCACTCTA 150
30 TT 152

(2) INFORMATION FOR SEQ ID :214:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :214:

122

TCTTCAGGAG AAGGGGCACC ACTGCTTTAA AAAACAATAC TCCNTTATAG 50
 ACTTGAACAT TTGCAGACAT TATGATCTTG CTTCCAACCTC CCACCGTATG 100
 5 TCCAGCAAAC TCTCGCATGT GGCCACTAGG AGGAATGCCG AAGAATGTTT 150
 ATATTACATA TTTATAACAT TAATAACTGG AAAAAGTGAA ATGCATGTCT 200
 GTTACAGGAA AATAGGCGAA TAATCAGATA TATATATCTA NNNCCGGGAT 250
 10 ATTATTCAAT AGTGGAATG ATGACTACAG CTATACCTCA 290

(2) INFORMATION FOR SEQ ID :215:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :215:

25 GTTCTTCCA GTACATCCAA GTTAAATTT ATTACGAAA TGGTCCATGT 50
 TTTTCAATT ACTGCTGACA CGATTCTAAG CTAAGTGAAG GGAAGATCT 100
 GAGAGCATGC TGTGTTGGACT GTTGATGCAT ATTCATGATG TAACAGGTCC 150
 30 TGGGCCTCAC TTTACCCCAT TCGTAAATG GGGATAATGT CACCTGCCTC 200
 TTACCTACCT CAGAGGGATT TCGAAGCAA ACTGTTAATC TTCGAAAACG 250
 35 ACCATTTACT TTAGGATAT CAA 273

(2) INFORMATION FOR SEQ ID :216:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

123

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :216:

ATCTACGGCT AGGGAGAAAC AATGTTCTTA CATATTATGG GTAGTGAGAA 50

CATTATCTGT ATAACAGGGA ACTGTGATTA TTAAAATTA TGCAGAACTT 100

10 ATTCATCTG TGCTTTAG 118

(2) INFORMATION FOR SEQ ID :217:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :217:

25 GAGGCTGGTG GCGAGGGAGT TGTGGAGGAT AACAGAAGA AAACAAGTCT 50

ATCACTAATG ACTTATTTTA CTTAGTTTCC ATTCACGAAA CCCTTTTAAA 100

TACAAGGCAA CATTTTCACA GCTGAAAAAT TACAATAAA NGNNNTGATT 150

30 TACCACCAA AGCAATAGAT GTAGTTATGT ATAATCTATA GATAATA 197

(2) INFORMATION FOR SEQ ID :218:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

124

(xi) SEQUENCE DESCRIPTION: SEQ ID :218:

CTCGCGAGCA CTCGTCCGAG AGGTCCCATATA CNNNNNNNCC CAAGCCCCTC 50
5 AAGGGCCTTT GCCAATCTNG TCATTTTATG CCAAGTCCTC TAAACGCAC 100
TCAGGGGTAT CTACATCGCA CTTGTACAGA ATATCAAGAT CTTATCCTCC 150
TATTTTAGGC TNCNAGGTCA AAATAAA 177

10

(2) INFORMATION FOR SEQ ID :219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :219:

GAAATGAAAA AGAGAGCATT ATTGGAAGAA TGAAAAATAC ATCTCAGAAA 50
25 GAAACCTANT AGTTCAACAA ATTAAAAGAA AGAAAGAAAA AAAGCAAAAG 100
TNGGTNTCAG GGCTGGAC 118

(2) INFORMATION FOR SEQ ID :220:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :220:

GAGAGCCCAG CACGTCATCC CCTGATCTGA GTCTACTGAA CACCTGTTTT 50

125

ATGGACTACA CTGTCTTTTC CTTTGAATCC CCACTTCTCC TGGAACTGTA 100
CTTGGACCAC CAGGAACATC GTAAGACACA ACCCAATACA CTCACCGCAT 150
5 TCAGACAACT GTCCAGACAC TGCCCTGACA CCACAGGGNC CCCTTTACAN 200
NGGTTGGNGG AAATATNNTT TAATCTCAGG CCA 233

(2) INFORMATION FOR SEQ ID :221:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :221:

20

GCACACAGAT ACCATCCCAC CTTGCTTTNT GACAGGCCAG CCACACAATA 50
ACCCTTTCCC TACTCACTAA AGCATCCCTA GGACACCAAC AATGAGGACA 100
25 GGCAGACTTA CCCCCGCCAT CTAGAGAGAA TGTCGTTATT ACCCATAAAA 150
CTCGACCACC CCCATATNCA CTNTTGGGTA AAAACAAACG CTTAAACCTG 200
TGAGCCTGCC ATTCCTTTTT ACGTGTTAAT CAATT 235

30

(2) INFORMATION FOR SEQ ID :222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :222:

126

GCCAATNNNN NGGCGCGAGG GNNAGAGAGA ATGGCAAACA GGGACCCGGG 50

CCTTAGGAAT TGANTGAGGA CTAAATTTC CCCNGAGGGA GAGNAGTGGA 100

5 G 101

(2) INFORMATION FOR SEQ ID :223:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :223:

ACGGTGACTT TCCATCCCTT GAACCAAGGC ATGTTAGCCT TGGCTCCAGC 50

20

ATGTCGTCAC CATTCCAACC AGAAATTGNC ACAAATGCTA CTGGTCGGGT 100

TGACCAATTT TCTTAATGAA GTGCTGACTT CCTTAACAAT TTNTTATATT 150

25

TNTTCGACTG TAGGGCGCTC ATGAATCCAT TTCGTTAACA CCGACAATTA 200

ATTGTTTCAC ACCCAGTGTG CAAGCCAGAA GGGCATGCTC TGGGTCTNCC 250

CATTCTTGAG ATACCAGCTT C 271

30

(2) INFORMATION FOR SEQ ID :224:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :224:

127

AGTATTATTT ACTNGGTCAT CTGGGAACCT TAATGTGATT TATTTTGACA 50
ATTACTGTGG CACATGTTTA ATCTGCAGCT CCTGGCGACT ACTGTGCTTA 100
5 T 101

(2) INFORMATION FOR SEQ ID :225:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :225:

TTCATTCCCT CCAGTGCNCG NNCATGCGAC ATATACAGGN NNTGTACCGT 50
20 AGGCGCTANT GTGTGGTACT CTGCCACGNN ANACCNCNNC TCGTCTTGAA 100
GACCCTGTTA ANTTTGGTGA AAATAACTTT CCANATTTC A 141

25 (2) INFORMATION FOR SEQ ID :226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :226:

ATTTTCTTAT ACTCCTCCCA CAGATGAGTT CACAAATACA AAAANTGGTG 50
TACATTTATA CTCAAGNACA AATCTCCAAC AGCCAAGTAA TTATAGTTTG 100
40 TTCTGTTATG TGCAAAGTAG ATTATTTTCAT ATTTACTTGG TATGGAAAGC 150

128

AGAGTACAGG CTCAATGGAC AATAATCATT AAACACACAT TATNTTTAAG 200

AAAANGCTGT TNNA AAAA 218

5 (2) INFORMATION FOR SEQ ID :227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :227:

GAAAACTTTA TTTGTCCACA CCAGGATTAC CGAACAGAAN NACNNGGTGG 50

TGAGAAGTTG GTATTNATAG CACCTTATTT ACATGATGGA CTTGAGGAGG 100

20 CAGTTAATCC TATGGTTGTG TATCACAACC TTTTATTAGC AATGCCATCT 150

TCGTCTTGCC TCCNCCCTAC TTGAATATCC CTTACGGTCA ACANCCCNCG 200

25 GGGTTGGGC 209

(2) INFORMATION FOR SEQ ID :228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :228:

TTTNNCAANC CAAATGGTTA TTTATTCTAA AACTGGAAGC TACTTTGCCT 50

40 ANCATTTTCG CCAGAATGGT GTAATGNNNA CAGGGGAGGA AAAAAGTTAC 100

129

AGATGTAAAC AATGACACAG TTACATTTTT TTTTAAATG GTAAAACCCC 150

TTTTTACTGG NCNTTCCAGA ANCTTACAG 179

5 (2) INFORMATION FOR SEQ ID :229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :229:

AGTTTAATCT CANNNNNNNA TGTCAAGT TATTGTAGCA GTGAAACAAT 50

GAGGGCATACTACTATATNGA AAAAAAACC TCCTCCCTNA TTCTCAGGCC 100

20 AACCACAGGC TTCTGCCCTG CAAAGATCAC CAATGTCAAT AGTTTGGTAA 150

TACACCATCA TAAAGGNTCC TAAATTCATC TCTA 184

25 (2) INFORMATION FOR SEQ ID :230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :230:

GAGACAGATG TANNNAAAGT TCAGAATACA ACAGTTAAGA CTCAGTTTTTC 50

TTTTTAGGTT TAGAATTTGA GAGCAAGTAT TGNTATGGTG AGCTGTTTTA 100

40 GTGCAAACAT TGTGAGTAT GTTGTCAAAC GTCTAAAAA 140

130

(2) INFORMATION FOR SEQ ID :231:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 178 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :231:

CGGAGACTTG TCCAGAGAGT TGTCTCTTNT NNGTTGGGGG CCGTCCCGCT 50
 15 CCTAAGGCAG GAAGATGGTG GCNNNTNNG ACGAAAAAGT CGCTGGNGNN 100
 NATNAANTNT AGGCTCNAAN TNNTTATGAA AANTGGGAAG TAANTNNTCG 150
 GGGGTAAAAG NAANATNNGA ANATGGAT 178

20

(2) INFORMATION FOR SEQ ID :232:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :232:

GAGCCAACGC CACNNNNNAG NTGAACCACA CTCACGAAAA AAACNCNTAC 50
 35 CGTCGTCNTA ATACNNANTC TTCCCATACA AAAATCGTCC NTNTAAATNT 100
 NNTAAACCAA TTCACAGCCC ACAGAACNAA TCAGTAATTT TATANCTTCN 150
 NCGAAACCAC ACTTATCCCC ACCTTGGTCT ATTCATNACC CGGATNGAGG 200
 40 GCAACCANGG 210

131

(2) INFORMATION FOR SEQ ID :233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :233:

5	ACTGTGCGAG TAGCTTAAA ANNNNNNNNN NNACTCAGTT TNATTATAC	50
15	AAAAAGAAAG GGGTGTGNAG TCCATGGTGT TGTACAGTNT NTAATTAGNC	100
	CANNACGAGA AAANANATNN NNNTNNNAAA NNNTGAATTA TGGGGTNAGG	150
20	ACTNTCTNAC NTTCAAACNA NTATTNCACG TAAAAACAT CACAGTGCGA	200
	AGAAAGNNAN CNCANNTAGA GCANGAAGAC ATCAAAAGCC AGCCGGG	247

(2) INFORMATION FOR SEQ ID :234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :234:

35	AAACACCAAA NAAANNNNNC NAGCAANAAA GTGGAAGACT AACCAAGATT	50
	GTGGACATTG GAATGTTTAC TGTATTCTG TGTAAAGAAA CAACTNACAA	100
40	AAAAGAAAAA TGGNCAACAA AATTGTTTCC CGGCNAGGCT GNAGGAAACC	150
	NGGGGGAAAN TGCCNGGGC	169

132

(2) INFORMATION FOR SEQ ID :235:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :235:

GCANCACANA AAGGAGACGN NANAGCAACG CAGAGATAGC CATCCAGATA 50

15

G

51

(2) INFORMATION FOR SEQ ID :236:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :236:

CAAGTGTAAG TGCTTGACCC TCTCTNCCTC CCCGANTGAA CTCTCTGATC 50

30

TCAAACTTTT TTAGGAAAGC CAGATTAAAA GCAGACGTAC CTAAATNCAA 100

A

101

35

(2) INFORMATION FOR SEQ ID :237:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

133

(xi) SEQUENCE DESCRIPTION: SEQ ID :237:

5 CATTATAAAA CAGCCTAACT TCCCTTATGC CATATGATTG CCTTAAAAAG 50
ACCAGATCTC AAGGAAAAGA TCATCAAAGA GCAGAGATCT TGAAGCGGCA 100
CAGTTTTCCA GCAGTTTTTCG TATTNTTTTT TATTACGAA TGCCATACTC 150
10 TGTTTT 156

(2) INFORMATION FOR SEQ ID :238:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :238:

GCAGNCTAAT TGTGAATCTA AGAACTACT CATAGACATC CCACCCTAAT 50
25 GATTTTACCT NNAACNTTTC TCCTTCATCA TAGAACCTTA GCAACATCCA 100
CCTCCTGTAG CACGAAACGA ATCAACAAC CCCCTGGATA ACCTCTCA 148

30 (2) INFORMATION FOR SEQ ID :239:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :239:

GAGTTTAAAC TTAATCACCT CTTTAAAAGA CCTGTCTCCA AATACAGTTA 50

134

AATTGAGGT ATTGAGGGT AGGACTTCAA CATGTGAGTT TGGGAAGGGA 100
 AGCACAAAAT CAGCCCCTAC CATGGTATAT TTATCATTGA TACATTACTA 150
 5 TCAACTAAGC TCAAGATTTT ATTCAGATTT GACTAGTTTT TCCACTAAGG 200
 CCCTTTTCT TTTCTAGGNT CCCACAGAGG ATACATTACA TTTACTTACA 250
 TCTTCTCT 258

10

(2) INFORMATION FOR SEQ ID :240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :240:

GAGCATTATT TGATGCAGAA GTTGAAAAC AATAGACTCA AGAAAGAAAA 50
 25 CAAACCAGTG ATTCCCCTTC CTCAGATACT GGGACTAACA GCTTCACCTG 100
 GTGTTGGAGG GGCCACGGAG CAAGCCAAAG CTGAAGAACA CATTTTAAAA 150
 CTATGTGCCA ATCTTGATGC ATTTACTATT AAAACTGTTA AAGAAAACCT 200
 30 TGATCAACTG AAAAACCAAA TACAGGAGCC ATGCAAGAAG TTTGCCATTG 250
 CAGNTGCAAC CAGNGGAGNT CCTTTNAAGN GNAACTTCTN GNATAATNNC 300
 35 AAGGGTNAAC NTNTTTNNA ANNNGCCNAA NCNNGATTTT GNACNCCCTT 350
 TNNCATTGGC ATTNANTGAA AAAAGTT 377

40

(2) INFORMATION FOR SEQ ID :241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs

135

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :241:

GGNGCACTGN TCCGAGAGCT TTTTNTCTG AAGAATAGCA TCTTTAATGA 50
10 GTGTNCTAAT CCTTGTCATC TGAAGTTTGT AAATATATTT CCCAGGGTCA 100
GAACAATACA GAGA 114

15 (2) INFORMATION FOR SEQ ID :242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :242:

CTCAAAATNC TGTGACAAAT TTNNNNGGTC AAGTTGTTNN CCATTAAAAA 50
GTACCTGATT TTCAAAAACC TAATAACCTT AAAACCNCCC CACGNAAAAA 100
30 AAAAAANCNA AAGNGGGCCC CC 122

(2) INFORMATION FOR SEQ ID :243:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

136

(xi) SEQUENCE DESCRIPTION: SEQ ID :243:

50
GAGAATGGGA AGCCTCATT TGGGGACAAG AACCTGTACA AGGATTTGTG
5 ATGAACTTTT CCAATGGGGA AATTATAGAC ATCTTCAAGC CAGTGCGCAC 100
NTATGATATG CCTCATGATA TTNTTGCATC TGAAGATGGG ACTNTGTACA 150
TTGGNGATGC TCATCCAAAC C 171

10

(2) INFORMATION FOR SEQ ID :244:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :244:

50
AACTTTACTG TCAGATAATA AAATTAGGGC TTTCTCTTAA AGGGCTTCTT
25 TAAGAGAAAT ACAGAGTGTT TGGTATNTGA GAGAAAAAA GTTAAACAG 100
GACTTTCAAC TTAATCCAGA CTTCCTAACA GTGTTTACAT GTGAGGGAAA 150
CTCCTTTAAG TAATGCGTAG TGTTTTATTT TTACCATCAT TGGNGACAAA 200
30 AAAACAAAA ACATAACAT CTNANGTGAA ATATA 235

(2) INFORMATION FOR SEQ ID :245:

35

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

137

(xi) SEQUENCE DESCRIPTION: SEQ ID :245:

	GGCCTAGCCT GCCATACCCT TACGAGCAGG CTCAGTGATT AGACTTTGAG	50
5	TCTAAGTTAA AAACGCCCTG CCCCCTTCTC GCAGGCCACC TACACCGTNN	100
	TTTTATCGAT TTGATAAAAC CACCAGCCTA CTCATCAAGN NGCACCCTGC	150
	NTNTACNTCT AACCNATAACA TNACNGCGGC CACCTACTCA TGCCCTANTG	200
10	CAGCNCACCC T	211

(2) INFORMATION FOR SEQ ID :246:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 194 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :246:

25	GGCTGAGAAT CCTTGAGCTT ACCATTTGAT ATTTCTATAT TATTTAAGAA	50
	AAGTCAAAAG ATTTTGAAAA CAGCAATAGA AGTAAGATCC TTTAAGCTCT	100
	ATTGTCAGCC CCTAAGAAAA GTGATGAGGA CACTGTGCAT GCCCATATGT	150
30	GAACATGGTG GTACCTTAGG NATTTCCCTT TNTCNATGAA TATA	194

(2) INFORMATION FOR SEQ ID :247:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

138

(xi) SEQUENCE DESCRIPTION: SEQ ID :247:

	GGCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT	50
5	GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG	100
	CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT	150
	GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA	200
10	GGCCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCCT	249

(2) INFORMATION FOR SEQ ID :248:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :248:

25	GGCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT	50
	GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG	100
	CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT	150
30	GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA	200
	GGCCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCCT	248

35 (2) INFORMATION FOR SEQ ID :249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

139

(xi) SEQUENCE DESCRIPTION: SEQ ID :249:

5 GGAGGGGACC GCAGCATCCA GCCCTCTAAG GCCGGGCAGC GGTCGCGTTG 50
GGGCAGAGCG CAGCGCAAGC AGGCTCAGTG TA 82

(2) INFORMATION FOR SEQ ID :250:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :250:

20 GGGGCCCTCA GGACATCCAC GTGAGCGTCT GCCCAGCTGC ACTGATATTG 50
TNTTGCAAAT CCAGATTTGT TGNCATTACT GATGGGCGCG TGAAACCAGN 100
GAGAGATGCA CAAGATTTAC AGGCC 125

25

(2) INFORMATION FOR SEQ ID :251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :251:

GGCCCAGAGG TCCTTTACTC TTACGGNACA CCTTAGCCAC ATTCACAGGG 50
40 AATGNTCCAG CACTCAGGCT CCTTCCCATN GGTTTTCAAA AGCGCGTTTT 100
TCTGGGGGAG CGGCCGCCTT TAGTCGACCC 130

140

(2) INFORMATION FOR SEQ ID :252:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :252:

GAGAAGGCTG GAGAAAAACC ATCCACACAT AAACAATNGN ATTTACTCNA 50
15 AAATNAAGTA CAGGTTTCAG GTATTTAAAA TAAATAAAGA AAAATCTCGT 100
TTCCTTTGGC ATCTTTAGAA AATAAACTAA GCAATAAAAG AGGTGATTGT 150
ATAAAGACAT GCGTAAGCAA ACATATGGGG AAAACCAGCA ACTTGTTTTT 200
20 ATGNGATAAT ATCAGC 216

(2) INFORMATION FOR SEQ ID :253:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :253:

35 GGAGAAGGAG GCTGATTGCG TACATCCAGC AGTTACAATT TTAAAAAATT 50
ACANTNNNNC NNTTNGATTN TTAATNTANG TAATTCCTT CCAAAGAAGN 100
TTCACATGTA ATAAGTAGAA ATTCTGTATA GGAAAAAAGC ATTAAAAATA 150
40 TANATACNGC TTCATNCGTT GGGAACCATT AAAAGTAATA TAATNAGCTT 200

141

TTTTCAGAAG GATCTTTTGT AGCAGTGNTT ATGAATGNAC CCGCAAAAT

249

(2) INFORMATION FOR SEQ ID :254:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :254:

15

GACCCCATTC TATATTATNC GTNNGCGAT TTTTAGCCA CCCTGAAGTT

50

ATATTTNTAT ACCNAGGCTT CGAATAATCT CATCNGACTN ACCACCCTNG

100

GAAAAAAGA ACCGTTTGAT ACATAGGNAT GNTNAGCTTG ATATCAATNG

150

20

CTCCCTGGGN TTCTTG

166

(2) INFORMATION FOR SEQ ID :255:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :255:

35

CCAGACCAAC CGCCTGCAGG AGGCTCTGAA CCCTCTTCAA GAGCATCTGG

50

AACAACAGAT GGCTGCGCAC CATCTCTGTG ATCCTGTTCC TCAACAAGCA

100

AGATTTGCTC GCTGAGAAAG TCCTTGTTGGG AAATCGAAGT TGAGGACTAC

150

40

TTTCAGAATT TGCTCGCTAC ACTACTTTGA GGATGCTACT CCCGAGCCCC

200

142

CTTCTNTTGT NACAGACAGC AGA

223

(2) INFORMATION FOR SEQ ID :256:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :256:

15 GGAGAAGAAG GAGCAGGAGG TGATGCTACT GACTCAAGTC AAACAGCTCT 50
TGATAATAAA GCTTCATTGC TCCATTCAAT GCCTACTCAC TCCTCTCCGC 100
TCTCGAGACT ATAATCCATA TAACTATTAA GATAGCATCA GTCCCTTCAA 150
20 CAAGTCTGCC CTCAAGGAAG CCATGTTTGA TGATGATGCT GACCAGTTTC 200
CTGACGATCT TTCCCTAGAT CATTCTGACC TGTGTAGAG TTGTTGAAGG 250
25 AGCTGTCTGA CCATAATGAG CTGTAGAAGA AAGAAAAATT GC 292

(2) INFORMATION FOR SEQ ID :257:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :257:

40 AAGGAGCAGG AGGTGATGCT ACTGACTCAA GTCAAACAGC TCTTGATAAT 50
AAAGCTTCAT TGCTCCATTC AATGCCTACT CACTCCTCTC CGCTCTCGAG 100

143

ACTATAATCC ATATAACTAT TAAGATAGCA TCAGTCCCTT CAACAAGTCT 150
GCCCTCAAGG AAGCCATGTT TGATGATGAT GCTGACCAGT TTCCTGACGA 200
5 TCTTTCCTA GATCATTCTG ACCTGTTGTA GAGTTGTT 238

(2) INFORMATION FOR SEQ ID :258:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :258:

GGAGAGAAAA GTTCCTGAGT GACAGAGAAA AAGAACAAAA AGCTGCAGAA 50
20 GGCNTCAGCA GAGGCCACTG CTGGCCCTGA GGCTGCACCA AGTGACGAAG 100
AACCGGCTCC AAGCATTCGT CACAGCACTA ATTTAAA 137

25 (2) INFORMATION FOR SEQ ID :259:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :259:

GCGCGACTTT TAAGGGATTT GCNGTGATGC CTGTTGACCC AGTGCCTTCC 50
TAGCCGGGAA GGGGCTCGGC TGGAGTGNN AAGGCTCAGAA AAATTCGCG 100
40 AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150

144

TTTTGGACAG GTGGGTGCGG TGACCTTGGT ATGTATTTTT CGTGTTACAT 200

CGCGCCATCA TTGGATATGT TAGTGTGTNG GTTAGTAGGT C 241

5 (2) INFORMATION FOR SEQ ID :260:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :260:

GCGGACTTTT AAGGGATTG CNGTGATGCC TGTGACCCA GTGCCCTCCT 50

AGCCGGGGAA GGGGCTCGGC TGGAGTGNA AAGGCTCAGA AAAATTGCG 100

20 AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150

TTTTGGACAG GTGGGGCGGT GACCTTGGA TGTATTTTTC GTGTTACATC 200

25 GCGCCATATT GGTATATGTT AGTGTGTTGG TTAGTAGGTC TCGTATGA 248

(2) INFORMATION FOR SEQ ID :261:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :261:

GGATCTTTCA GGTGATGAAA TAGTTCTGTA TCTTGATTTT GGCGAATCTA 50

40 CACANGTGAT GAAGTAACGT GATAAAATGA CATAGACCTG TATGCCTACT 100

145

ACAATACAGT ATCAAAACCA GGGATTGATT CCTGGTTCTT TTCCAAATCC 150
 ACTTCCCAA CTTATGGTAA GGTAATATTA AAAAGGCACC AAAGAGCCCT 200
 5 GATCCCTGGA TAAACAGGAT CATTCAAAG NNGTTTATA 239

(2) INFORMATION FOR SEQ ID :262:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 143 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :262:

GCCGGGTGAT GGCCAGGAAG GTGCCCTCTG TTTTGTAA AACAGCCATT 50
 20 GGCCTTTGTC ATTGAGTCAC CACCTGCAGG GCTTGGGAGT GAGCGTTGGG 100
 TAGGNTCAGG CCCCCAGAAC CGCCTGGGTA CTCACCGCTA GCA 143

25 (2) INFORMATION FOR SEQ ID :263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :263:

GGCGCTCAGC CTCCCCAAGG ACAAGCTCCT CCCCCTGTAA TACCTCCTCC 50
 TAACAGCCGG ATATGGATGG CAAGTTACCA AACACAGTGA GCCGGGACTC 100
 40 TAAAAAATA TAGCAATCCA GATAGGCTTC GATTTCCTGT GACACTCTGA 150

146

AGACATGAAA GTAGACATCG AAAATGAAAA TANTTATNNA AATGAAATGT 200

TTGGAACCTT TAGCACAGAT TTGTTTGGGA AGACACGGTC TTTTAG 246

5 (2) INFORMATION FOR SEQ ID :264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :264:

GGCTCCATTA AGGACCAAAT TNATGCTACC ACTAAACAAA AANNTATAGT 50

CTGTGTTAAA TCGTATGCTT TTAAAGGTA TTAAAGATT CAACTAGCTT 100

20 TAAAGAGGCT GAGCAGCTCA GGAAGCCTGT AATGTGACAT AACTCTTTGG 150

ACCTGATCTT GATGTTCTGC TGTGTNAGT CTTGAAGAGC GATNTGAT 199

25 (2) INFORMATION FOR SEQ ID :265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :265:

GGTTTCAATC GTCCATCCAA GATACAAGAG AACGCATTGC CACTGATGCT 50

TGCTGAGCCC CCACAGAACT TAATCGCCCA ATCTCAGTCT GGTACTGGTA 100

40 AAACAGCTGC CTTCGTGCTG GCCATGCTTA GCCAAGTAGA ACCTGCAAAC 150

147

AATATCCCGT GTCTTCTCTN TCCCAACGTA TGAGCTGCCC TCCAAACAGG 200

AAAAGTGATT GAACAAATGG CAAATNTTAC CCTGAACTGA AGCTG 245

5 (2) INFORMATION FOR SEQ ID :266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :266:

AGGAAAAGAT GGGAATATGT TTCTTTCCTT TGAGAATTCA CAAAANGGGG 50

TCAAAAACAA AGCAATGCTG AAAGCGAACA TCCATTNGC CTGCAATTCA 100

20 AGGCGAAAAT CCAAAGGCAT C 121

(2) INFORMATION FOR SEQ ID :267:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :267:

35 GGGTCGCTCT CCCCCCTCT TTCTTCGGGT TGTGTGCGTC TCCGCTTTCG 50

TGATGTGAGG AACTCTGGGG TGGGCGACGG GTCCAAC TCG CGTTGTCATC 100

TCCCAGGTG GTACACCCCC CCCCCGTTTC CCCAGCCACA CTCCACGGCC 150

40 AGGGTGGAGG CAGATGTCT 169

148

(2) INFORMATION FOR SEQ ID :268:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :268:

TCGCAGGAGA GGAATTACAT GCTCATCCTA GAAGGGGGGG CTGACTGCAG 50
15 GTGTTGCTGG GAAGCCTCTC CAGGCCTGGA GCTGGAGTAC CCGTCCTCAG 100
CACTGCCAGC AGAAAAAGTT GTGATTCAAG GAAAGCACAT TGAATGCATT 150
20 ATAGCAATCC CAGACCTAAG TTCCAAGTTG CTTTGTAAAC AGTGCTGCCT 200

(2) INFORMATION FOR SEQ ID :269:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :269:

AGGGGGGCGC AAGAGAGAAG AACTTCACAC TTCTTTATTG CTCAGCCTAG 50
35 ATAGCAGCAG CTGGGAATAC GTAGGACAAA CAGGACGTCG AACAAATTAC 100
TCCACTATAT TAATATTCAC TACACCACTT ATTCTTTCTT GAATTGTAAA 150
CACTAAGTGT AGT 163

40

(2) INFORMATION FOR SEQ ID :270:

149

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :270:

TCACACTTCT TATTGCTCAG CCTAGATAGC AGCAGCTGGG GAATACGTAG 50
GACAAACAGG ACGTCGAACA AATTACTCCA CTATATTAAA TTCACTCACA 100
CCACTTATTC TTTCT 115

(2) INFORMATION FOR SEQ ID :271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :271:

CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA 50
GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNGGN 100
NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC 150
TGCAGAAATN CCTATGTGAC TCTTATAA 178

(2) INFORMATION FOR SEQ ID :272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

150

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :272:

CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA 50
GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNNGN 100
10 NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC 150
TGCAGAAATN CCTATGTGAC TCTTATAA 178

15 (2) INFORMATION FOR SEQ ID :273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :273:

CTCTAGTAAA AATGTTTGAG GAAACAAAAA TGGGGAAGAA GATCAGAACA 50
AAANATTGT TAACACTGAC CGTCCTCATG CAGGTAGGCT ACTACCAACG 100
30 CTGGTTGTTA CTCCAGGAAA ATCGAGGTGA ACATC 135

(2) INFORMATION FOR SEQ ID :274:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

151

(xi) SEQUENCE DESCRIPTION: SEQ ID :274:

	TGTCGAGGAG AAGAAACCAC TTGATAACAC CCCGCGACAT CGTGGGGCTG	50
5	CTTGTCACAN GAAAGCACCA TGTTGCAAT GGATTGCTGC AGGTGCTGCC	100
	GTTGCCTCCT CAGGGTCTGC TGAAAGTCAT CTTCTAGGGT CTGAACGACA	150
	TAACGCAGGA AAAGGACTCG CCCAGGCAGA GTTGTCCCT CTCCTTCAT	200
10	GACATAGGTG AGCAGTTTCC AGTCCCACTC C	231

(2) INFORMATION FOR SEQ ID :275:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 170 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :275:

25	TCGCAGGAGA AGAAACCTNG TTGCTCCACA ATGCAACCAC ACTGATTTTC	50
	TCTTTTCTCT NNAGTTNTCC TTGTCTGTAA CAGGAATGTC CCTTACTATA	100
	GCAGGCGGAC ACGGCCATGG GTCAAGCACC CTGCTTCTGG AACTTGNNNG	150
30	NCGTNCCCAC CATTGATTGA	170

(2) INFORMATION FOR SEQ ID :276:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 315 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

152

(xi) SEQUENCE DESCRIPTION: SEQ ID :276:

5 ATATGAAGGA GGAAATGGCT CTCACCTTCG TGAATACCAA GACCTGCTCA 50
 ATGTTAAGAT GGCCCTTGAC ATGAGATTGC CACCTACAGG AAGCTGCTGG 100
 AAGGCGAGGA GAGCAGGATT TCTCTGCCTC TTCCAAACTT TTNTCTGAAC 150
 CTGAGGGAAA CTAATCTGGA TTTACTCCCT CTGGTTGATA CCCACTCAAA 200
 10 AAGGACACTT CTGATTAAGA CGGTTGAAAC TAGAGATGGA CAGGTTATCA 250
 ACGAAACTTC TCAGCATTAC GATGACCTTG AATGAAAATN GTACACACTT 300
 15 AGCGTAGCAT ATTNA 315

(2) INFORMATION FOR SEQ ID :277:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :277:

30 ACGTTCTGCG CCTTCCTAGG AGAGTCTTAC AGTGTGAGA TTTCACAAGC 50
 AATGCGAGTG TAAAATACCA GCTCTACAAG AAGCTAGGCT CTGTGACGGC 100
 ATAGTTTTCA GTAGCTTTAT CACAATGAAA CGAGAATTAT ATGACATGGT 150
 35 AGCAGAAATA GGCCCTTTTCG TNGCTGTTT TATTTNCTCG GATNGTAGAT 200
 ATAGTAATC 209

(2) INFORMATION FOR SEQ ID :278:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs

153

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :278:

AAGACATCCT AAGCTATGTT GAGGAGGGAG AAGATCTGAG ACTCAAGTTC 50
TGCTGTTAAC CATGAGGTGA TTTAGTAGCT AAGTACGCCT TAGCCTTTTA 100
GAGTCTT 107

15

(2) INFORMATION FOR SEQ ID :279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :279:

ATGAAGAGAA AACCATCCTC CCATATGAAA ATATTTGCAG TAGGAGAACA 50
CAGTGCAATA GGCTCCAAAA ATGGCTTTTA AGACCTTTGG NGGGGCAGTT 100
ACTACTGCTT TAAAGCCAG GTTAAAGTAT ACTCTAAGCA AAGATGACCG 150
TAGAGCAGCT AGCTTCCTTT TCTATAANNA TAGGGAAAGC TCTCTCCATC 200
GTCCATCAAA TCAGCTCTAG AAGGTTTTTC TTTCCCNCT ATAAGTGCAC 250
AAAGGGGAAA CACTGATTTC AAGCTT 276

35

40

(2) INFORMATION FOR SEQ ID :280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs

154

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :280:

AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA 50
10 CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT 100
TAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA 150
15 GTGTTATAAG TTGAAAAGAA CTCAAACAA CCAAT 185

(2) INFORMATION FOR SEQ ID :281:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :281:

AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA 50
30 CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT 100
TAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA 150
35 GTGTTATAAG TTGAAAAGAA CTCAAACAA CCAATA 186

(2) INFORMATION FOR SEQ ID :282:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

155

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :282:

TGTGGGCTCA GTAATGTCCC CGCTGATGAC AATTTCGAGA GTCCATGTTC 50
TATAGAAACC TTGAGGTCGG CCAGCCGTGT CTTGGCCAAT GAGATGTAGT 100
10 TGTGAGGAGG GGGCGTACTT GGGGACCAGG GGTGGGTGGA GATGTGCCCT 150
GTAGGCACAG GGAGACTCAA AAGCACGAGT TNTGAAAGCG TAAATGGG 198

15 (2) INFORMATION FOR SEQ ID :283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :283:

AGAAAAAGGT GAAGCGAAGC CCAAGGACAC CATGCTAAGG GCAAAAGTAA 50
GAGACAGTCT CAGAACTGAG AGAATCGTGT CTTCTGCTTT TTGAAGTAGA 100
30 CTGTCACACT CAGGCAGCCT GTCAATGCTG AATGTTAGGA CTTCTGTCTC 150
CGCTGGAGAC ACGCCTGGGC AAGTCAGCGT TTAGTGTTTG ACAGCTTTCT 200
35 CAGCTCCCTG ACTCCGTTTA CC 222

(2) INFORMATION FOR SEQ ID :284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double

156

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :284:

ATGGATCAAA CTACCTCTAT AATGAAGACT GTTCTCAAAA ACGCGAGGNA 50
ATGTGNGACG AACTGACCT ATCAGACAAG AGGGCATGCC CCCCTGGCCA 100
CCTTTGNCGC TGTNTGCA ACGTTCGCAG TGNTACTCTG CGTGAACCGG 150
TAGACTGCTT GG 162

15 (2) INFORMATION FOR SEQ ID :285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :285:

GGATCCANGC AAAGCCCACT CCTCCAGGGT GAAGTTTTTC TCCCGCGACA 50
GACAGCAGAC TCGAGCC 67

30

(2) INFORMATION FOR SEQ ID :286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :286:

157

GGTCGGATCA GGTCAACCCGG CAGCAGCAGC TCTCGAGAGC TGAGGCACAA 50
GGCAGGGGCC CGGCTGTACA CCTGCAGGAC CCAGGAGAGC CTGTTGCAGT 100
TCTTGTCGGA AGCGCCGAGA TAGCCACTCA GTGTCCCTGC AGCAGGAGCA 150
GAA 153

(2) INFORMATION FOR SEQ ID :287:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :287:

20

TACTACGGCT AAGGAGAAAC AATGTTCTTA CATATCACGG GTAGTGAGAA 50
CATATCTGCA TAACAGGGAA CTGTGATATT TAAAAACAGC AGAACTTATT 100
CCATCGTGCT TTAGAAATAA CTGTATACAG TGTATAAGT TGAAAGAAC 150
TCAAAATAAC TGATATAAAT ACATCTATGT ATTAGAATTT AAAAAAGCTG 200
CTTTCTGTGA AGTCAATCAG CTATATTAAA AATGACACAA ATCCAAACC 250
GATGCATGCC ATATANAAGG GACATTGNAA GTCCGCTCGC TGC 293

30

(2) INFORMATION FOR SEQ ID :288:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

158

(xi) SEQUENCE DESCRIPTION: SEQ ID :288:

5 AGGGTAAATG TACGTTGTTG AGTCACAGGC CTGCCAGACC TCTACTACCT 50
 CATTGTCCCC TCCGGTGACC AGTTCTGCCG TCACTGTCAG GAGAATGCCC 100
 GTGTTGAATC ACTG 114

(2) INFORMATION FOR SEQ ID :289:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :289:

20 ATGAACCACT GCCCGAGGTA CCCGGGTGTG GACCAGAGAA GTTGCTGGA 50
 AAGGACGTTG CCAGGACTTA CACGTTTACA GATCCAGCAA CTGCTCTNCC 100
 25 CAGTGCCACA ACCATGGGGC GCCAACCACA AGCAGGAGTG CCACTGCCAC 150
 GCGGGCTGGG TCCCACCCNA CTGCGCGAAG CTGCTGACTG AGGNGCACGC 200
 AGCGTCCGGG AGCCTCCCTG TCCTTGTTGTG GGGTATGGNG CTCTGGCGTT 250
 30 GNGCTGGTTA CCCTGTAGGA GTTANTGNCT ACCGGAAGCT 290

(2) INFORMATION FOR SEQ ID :290:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

159

(xi) SEQUENCE DESCRIPTION: SEQ ID :290:

5 AACCGCTCTC CACACCGCTC CCACGAGCTC CAAGCTTAAA CGTCCAGATN 50
NACTTTGTTG CTTTGCTGAT TTTAACAGCT TGATTCTAAG CNCTTACTAG 100
TATCATNTGT GGCAGGACTT GNTCCATATC AGTGTTACTT TTGCTACTGT 150
TTTGTAGAAC GATGTACATG AATGAGCCT 179

(2) INFORMATION FOR SEQ ID :291:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :291:

TCTTTCATTT TGNCTGCCAA TCATTGTCAG AAATTAGGG AAGTCAATTG 50
25 TGCCATTACC ATCGGCATCT ACTTATTAAT TATGTCCTGT AACTCTGCTT 100
CTGTGGGATT CTGCCCAAGA GATCTCATT CAGTTCCCAA TTCTTTGTTG 150
TTATAGTACC ATCACCATT CGTTAAATAG TGAAGAGCT TTTTGAATC 199

30

(2) INFORMATION FOR SEQ ID :292:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :292:

160

5 GGAAGACCAT TCTGATCATC CTCACTGACG CCP GGCAA GAGGGTGGTT 50
 TTCCTGAAGC AGCTGGCTGT GGCTTATACT CGTGAAGTGA CCTCTGGNCT 100
 CAATTGAGTT CCTCAACGAA GACCACACCA GAAATTGTCA TTGCCACCTC 150
 AACCGAANNG ATATTACAAT GTAAAAA 177

(2) INFORMATION FOR SEQ ID :293:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :293:

20

ATTGGTTTTC CTCATCCACT GAGAATGCTG CTGGTTACTG CAAACGTTCA 50
 CCAACCANAG CTTTGGTCCA TACAGCTTTC TTCTAGATTN GGAGACTCTC 100
 AAGGACAGCA GGNGCTTTAA AATCCCTGGA CTGTGTTGAG AGGGCTTCTT 150
 TAGGCTTTTC ATGATGTGAA TAGCCAGTCA TGAACCTTGN GTCTGTTTCT 200
 TTTAGGCTCT TTTTGACGCA GCAGAGCCAT GCTATNGAAG GAGTGAGAAC 250
 CTATGCGAGN GACCCNGTGN TTGNACTTGC CAGGGAGCTT GGCCT 295

30

(2) INFORMATION FOR SEQ ID :294:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

161

(xi) SEQUENCE DESCRIPTION: SEQ ID :294:

AATGATCCTT TTTTCGCTCT TACCTATAGT ACAAGTCCAT GATACTACTG 50
5 CATATTTTAC CATTTTGNA A CTGTGAG 78

(2) INFORMATION FOR SEQ ID :295:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :295:

ATTCTGTACC TGTTCTGAAC CTCGCCATAA GGGACTTGCA GCTTCGATT 50
20 GCTAACCTGA AATTCTGCTG CTGCCATGGA ACAAGCCTGG GCTAGCTTGG 100
GGGAGGAGGA GAGACCATGT GGAGTAGAGC CAAGCTCTGG ACATTGAGA 150
25 GAGCCCGGTA ATA 163

(2) INFORMATION FOR SEQ ID :296:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :296:

AGCTTAGAGC GGAACGGGTT CCACGTGCGG TACTCCTGCT TCACGCCGCC 50
40 CTCGGTCACC GTGACGCGCC TCTCGCCGTA CACAGACTGG CCCGGCACCA 100

162

TGTTAGCGTG ACCAGCGCGT CCTCCGCCCC GCGTNAGATG AAGAGGCCCT 150
CGTGCCGGTG CGCTCCACCG ACACCACCAT GGCCCCCTTC 189

5 (2) INFORMATION FOR SEQ ID :297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :297:

GGAAACCAGC CCCTCACATC CTCCTGAAC TTCCTGTCCC CACTCACACA 50
AGTGGTCCGG TGTACCCTG CAGTTGGGTA TAGTCATAGG TACCATTGAT 100
20 GACGCCTTCT ACCTCGGCCA TGTAGGCCTT CCAGTCAACC TCTGTGTCTG 150
GAAGAAGACA AGATGATCTG GTTACTTTTG AGTCTAGAAC TTGTCTGCC 199

25 (2) INFORMATION FOR SEQ ID :298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :298:

AAAAGATGAT AAATCCACCC TCNTGCTCTT AAAATCCCAT AAACGNTAGG 50
CTCTGGAGAA ACAAGTTGTT CTGTCGAGCC CTTGCCATCA ACACACTAAG 100
40 CAATCATAGT CCCCCAGAGC ACNAGATACT GCTAATGACC ATTANATNTT 150

163

GTATCATCAT GCTGCCTCCT GCATTGAAT T

181

(2) INFORMATION FOR SEQ ID :299:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :299:

15 AACATTGTTT ATTCATCCAG CAGTGTGCT CAGCTCCTAC CTCTGTGCCA 50
GGGCAGCATT TTCATATCCA AGATCAATTC CCTTTTTCAGC ACAGCCTGGG 100
GAGGGGGTCA TTGTTCTCCT CGTCCATCAG GGATCTCAGA GGCTCAGAGA 150
20 CTGCAAGCTG CTTGCCCCAAG TCACACAGCT AGTGAAGACC AGAGCAGTTT 200
CATCTGGTTG TGA CTCTAGC TCAGTGCTCT TCCACTACTT ATATNCGCCT 250
TGGTGCCACC AAAAGTGCTC CCCAAAAGGA AGGAGAATGG GATTTTTTCC 250 300
GAGGCATGTA CATT 314

(2) INFORMATION FOR SEQ ID :300:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :300:

40 AAGAGTCCTG AAGGCATATC CAAGCCTGTT GTTCCTGCAG ACCTCATTAC 50

164

CACGCCAACA GAGAAGGCTG GACTGCTGCC CACATGCTGC TTCCAAAGGT 100
TTTAAGAACT GCCTAGAAAT CTCGTGTAGG CACGAAGGGC TTGAGCCAGA 150
5 AAGGAGAGAC AAGTGCAA 168

(2) INFORMATION FOR SEQ ID :301:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :301:

ACCCACATG CCCAGATGTC CACGNGCTTG CNATACGCCT CTTTGCAAAG 50
20 GACCTCAGGG GACAGGTACC TGGTGTGCCA GCGAAACCAA ACCATGCCTG 100
CTGGTTCCCC TGACCTCGAT AGCTAGGCCA AGTTTGCCAG CT 142

25 (2) INFORMATION FOR SEQ ID :302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :302:

AGAATTCGTA ACTCATCCTA GAGTGGGCAC ATTTTAGACA TAGCAGGCGT 50
GATGACCAAC AAAGACTGAA GTTCCCTATC TACGGAAAGG CATGACTGGG 100
40 AGGCCACAA GGACTCTCAT TGAGTTCTTA CTCGTTTCA GTCAAGACAA 150

165

TGCTTAGTTC AGATACTCAA AAATGTCTTC ACTCTGTCTT AAATTGG

197

(2) INFORMATION FOR SEQ ID :303:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :303:

15

AGAATTGCAA CTCATCCTAA GTGGGCACAT TTAGACATAG CAGGCATGAT

50

GACCAACAAA GATGAAGTTC CCTATCTACG AAAAGGCATG ACTGGGAGGC

100

CCACAAGACT TTCATCGAGT TCTTACTTCT TTCAATCAAG ACAATGCTTA

150

20

TTCAGATACT CAAAAACGTT TCACTCTGTC TTAAATGAAC AATTGAATTT

200

AAAAGTTTTT GAATAAATGA TGAAAATTTT TTAAC

236

25

(2) INFORMATION FOR SEQ ID :304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :304:

ATGTCATTCT CCTCATCCTC CGCATCTCCA CTGTCGTGCA CAAGGACCAC

50

CATGTTTCCT TTAGTTCCCA GCACACGGGG CTCTGCAGTA GTGAATGAAG

100

40

TCTAGCACAG CCACCGCCCC CATGCCCAGG CTCAGGAGCA CACTGAGGTC

150

166

GTCCACCAAC ACACCGGGTA CGTCCACCGA GCCTCTCCAC TGCTCTGGCT 200

TTAGGCCTCC CGTACAAACT 220

5 (2) INFORMATION FOR SEQ ID :305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :305:

AGAAGAAAGG ACACCATTAC CATCCATATT GACATCGCAT TTCCATAGAA 50

ATGCCAAAGA AAGAAGGTCC TGGGGTTTTT TATAGAAGCT CAAAAGNTC 100

20 AACCTTCGAT GCTATCCCCC AGCCCAATAC AAAATCAGAA AAAGC 145

(2) INFORMATION FOR SEQ ID :306:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :306:

35 AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50

TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG 100

NGNTGATATA AACAGATNNA 120

40

(2) INFORMATION FOR SEQ ID :307:

167

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :307:

10

AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50

TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG 100

15

NGNTGATATA AACAGATNNA 120

(2) INFORMATION FOR SEQ ID :308:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :308:

ACTGCACCCA CCCCAAGGCC ATGGCAGGGT ATGGAGATGT CATTATCAT 50

30

AAGATGGACA GATAAGCTGG ACCAATAATT AAGATTCCAG CAGAGGGTGA 100

GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAATGA TGGCAACGTC 150

35

TTGCCTTCCT GGGGACAGGG AGCCCTATTC AAANANAGTC ACATCTGAGG 200

AGCCGGGGGT TATAACATCA AGTCTGTCCT TGACCTCACA AAGCCAG 247

(2) INFORMATION FOR SEQ ID :309:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs

168

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :309:

AGGTAAGGTT GTCACGTGGA ACAACTGATA AAGGTCAGCT ATATATGTAG 50
10 AGCTATATAT GTGAGTCACA AGGTGTGTGA CATACGTGTA TACGTATAAT 100
ATGCGTT 107

15 (2) INFORMATION FOR SEQ ID :310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :310:

GGAAGACCTC GCTGGACATC CTGCAGGGCC ACATGGTGGC TCTGCTTGTC 50
ATTCTGGGGT CCACCCTCTC CAGTCAAGAG AACCCCGTC GGGTTTAATG 100
30 TATCAGGAAA GAGA 114

(2) INFORMATION FOR SEQ ID :311:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

169

(xi) SEQUENCE DESCRIPTION: SEQ ID :311:

ATGGCAAATA GGAAGAAGCT CAGTATCCTC CTCCCACCAT AACCCCACTC 50
5 TCCACTGCCT CCTGGACCAT AGTTTCCTCC ACTATACGGT CCCCCCATGT 100
TCCTGCTACC ACCAAAGTTT CCACTCTTTA TCGAACCGTA TTAGAAGGTC 150
GCTGGTTATA ATTTCCAAAA TATGTAATTT CCACTTCCAA ATCCTTTATA 200
10 GTTGTCAATA CCACCTCCGT AGCCCCCACC CTGTTGC 237

(2) INFORMATION FOR SEQ ID :312:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :312:

25 TNNTCCACAA CAGNGGGACT ACTGAAGACT AGAGAACGCC TCTGTGNGAG 50
TGGTGACAGAC AAAGACCTCA CTAAAGTGNG CTTAACAGAG TACTAGAGGA 100
GAGAACTTGG CAATAGCAAG TACAGACAAC TATGTGAGAA ATACTGC 147
30

(2) INFORMATION FOR SEQ ID :313:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

(xi) SEQUENCE DESCRIPTION: SEQ ID :313:

170

5 CACAACAGNG GGACTACTGA AGACTAGAGA ACGCCTCTGT GNGAGTGGTG 50
CAGACAAAGA CCTCACTAAA GTGNGCTTAA CAGAGTACTA GAGGAGAGAA 100
5 CTTGGCAATA GCAAGTACAG ACAACTATGT GAGAAATACT GCTCCCAAAG 150
G 151

(2) INFORMATION FOR SEQ ID :314:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :314:

20

GAAGGTTGTA CGTGGACACT ATAAAGGTCA GCAAATTGGC AAAGTAGTCC 50
AGGTTTACAG GAAGAAATAT GTTATCTACA TCGAACGGGT GCAGCGGGAA 100
25 AAGGCTAATG GCACAACTGT CCACGTAGGC ATTCACCCCA GCAAGGTGGT 150
TATCACTAGG CTAAAACTGG ACAAAGACCG CAAAAGATC CTCGAACGGA 200
AAGCCAAATC TCGCCAAGTA GGAAAGGAAA AGGGCAAATA CAAGGAAGAA 250
30 ACCATTGAGA AGATGAGGAA TAAGTAATTN ATATANA 287

(2) INFORMATION FOR SEQ ID :315:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

171

(xi) SEQUENCE DESCRIPTION: SEQ ID :315:

5 GGAATCAAAC GNCTCTATAA TGAAGATAAT GTTCAGAAAA CGTGGGTTCT 50
GTGGTGACAC TGATTTATCA AGACAAGAGG GACATGCTTC CCCTTGTTCCA 100
CCTTTGCAGC CTGTTTCTGT CATGTAGTTT CAACAAGTGC TACCTTGAGT 150
GTAAACTAAG GTAGACTACT CTGNGAATAA GAA 183

10

(2) INFORMATION FOR SEQ ID :316:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :316:

25 GGAATGAATC AAACGNCTCT ATAATGAAGA TAATGTTTCAG AAAACGTGGG 50
TTCTGTGCGT GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG 100
CCACCTTTC AGCCTGTTTC TGTCATGTAG TTTC 135

30

(2) INFORMATION FOR SEQ ID :317:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :317:

CGTTTGAAAT TCATCCCAAC TGTAGGCTGA GTGACCTGAA GTTGACAGAC 50

172

TGCCGAAGTC CAAAAGCTTC AGCATTCCT TAGTGCAGG ATCTACTTCA 100
ATAATNNTGA TCCAAGGCTG AGACCTCAGA AACATAATGC TCTCCTTTCC 150
5 CTATNTTTC TCGGCTTGA TGGAGATACC TTTACTG 187

(2) INFORMATION FOR SEQ ID :318:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :318:

TCCCAGGAGA AGGAACTTG AAATTCATCC CAACGTAGGC TGAGTGACCT 50
20 GAAGATTGAC AGACTGCCGA AGTCCAAAAG CTCAGCATT TCCTTAGTGT 100
CAGGATCTAC TTCAATAATN NTGATCCAAG GCTGAGACCT CAGAAACATA 150
25 ATGCTCTCCT CCCTTNCTTT TCTGCGCTTG ATGGAGATAC CTTTCACTGT 200
GCCTCTCTGA ATCGTTTCAT CAGATGCTGA CGTAACCTGC TATTTGTTGN 250
AGCTTTCNGT TGNNTAA 268

30

(2) INFORMATION FOR SEQ ID :319:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :319:

173

ACTGCACCCA CCCCAAGGCC ATGCAGGGTA TGGAGATGTC ATTTATTATA 50
AGATGAACAG ATAAGCTGGA CCAATAATTT ACAGATTCCA CAGAGGGTGA 100
5 GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAAT 138

(2) INFORMATION FOR SEQ ID :320:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :320:

AAATGATGAT AAATTCATCC TCTTCTGCTC TTAAAATTC ATAAACCTCA 50
20 GGCTCTGGAG AAACAAGTTG TTCTGTTGGG CCCTTGCCAT CAACACACTT 100
GTAATCATAC TTCCCCCA 118

25 (2) INFORMATION FOR SEQ ID :321:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :321:

AGAACAGTTG AAGGTCTGAG GTGTTGAGAG GCAAATGGGG TCTCTGGGTG 50
GATCCTGGTC CTGTCAGCAG GCCTGGACTT GTTCAGGATG GACTGGTGGC 100
40 GTTATAAAGG GCAGATCAGG GTGCCTGTCC CTTGGCATGT CCCTTAAGAT 150

174

TTCCTTTTCC

160

(2) INFORMATION FOR SEQ ID :322:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :322:

15	AGGAGGGAGT TAATCCAAAC CACACAATGA AGTCTTCAA CCACCNCCCG	50
	AACAGGGCTG CTGATTGTTC CTTTCACTTT TGNGGTGACC TTGAGCTCCC	100
	TTAAAAAAAA AACTTGGAGA ATCACAAC TGCAATGCACC GCAGTTCTCG	150
20	AACTACACAA GCATAGTCTG ACTAAGTCAC ATGTGTTTCC ATATCAACTT	200
	GTTTGACAGG GCGACCTACT GCAAAGCAGG CTCAGTTACC CCACCAGTCA	250
25	ACCCCTGGG AGTATAATNN TCTCCATANA A	281

(2) INFORMATION FOR SEQ ID :323:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :323:

40	GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC	50
	ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTG	99

175

(2) INFORMATION FOR SEQ ID :324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :324:

GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC 50
ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTGA 100
CACNNGTCCN NNGCNCNAGN TTACCATCCT TATGTGAATA CTNCAAGGGA 150
TTGCCCCGGT TTTTAGG 167

20

(2) INFORMATION FOR SEQ ID :325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :325:

TGATCCAACCT CTCCTGTGT GAAAAGAAGA ATGATGGCAG GAAGAACATA 50
AAGACTTTAA AACTCCTAGC CGGGGTTTGT CGGACTCTTT GNCAGTAGTG 100
ATTTAGCCAA CCAGGCAACA GAGATACGAT CTAATCTCCT CGCCCCCTCTT 150
TCGGGTCGCG 160

40

(2) INFORMATION FOR SEQ ID :326:

176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :326:

10

GGAAGGGGTG TTGTTTGATA GACATTATCT GTGGCTGGGT CTTTCTGGCT 50
GATGAGAGAC ATGTAGATTA TGTGAAGCAA GTGGCTAGAA GATGAGAGAG 100
AACATGAGAG AGCAGAGTGC TCTC 124

15

(2) INFORMATION FOR SEQ ID :327:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :327:

30

AGCCTAGTTT GAACATCCTC ATCCCNGTGT TAGACCGGAT CCGATATACA 50
GAGTCTTAAG GAAATCGCAT CAACGTGCCT GAGCAGTCGG CTGTGACTCT 100
CGACAATGTA ACTCTGCAA TCGATGGAGT CCTTTACCTG CCATCATGGA 150
CCCTTACAAG GCAAGCTACG ACGCGAGGAC CCTGATATGC CGTCACCCAG 200
CTAGCTCAAA CAACCACGAG ATCAGAGCTC AGCAAACCTCT CTCTGGACAA 250
AGT 253

40

(2) INFORMATION FOR SEQ ID :328:

177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :328:

GAACCTCTGG GCTCTCATCC TCTCCTATTG ACAGTGAAGC CCATGGCAAA 50
TAGAAGAAGC TCAGTATCGG CTCCTCCAC CATAACCGCG TTNAATCGC 100
CTCCTGGACC ATAGTTTCCT CCACCATAAG TCCCCCATG CTCCTGCTAC 150
CACCGAAGTT CCCACTCCTG NGCGAACCGT AGTTAGAAGA TCGCTGTTAT 200

(2) INFORMATION FOR SEQ ID :329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :329:

TGACCTGATC ATCCTGAAAA ACTTTATGGG GGAGAAAGGT CAGCAGCTTC 50
TCTTTCTTTT NTCGAAAATN ATAAACTGC GTATTCTACT TTATATTAA 100
TGTAAGGAAG AAAATATACA AGCCCATATT TACATCGTAT TTCTATTAAG 150
AGCAACAATA GTTCATATGT TCATGTTTGC TACTATCACA ATNCAACATA 200
TGAACACAGA TCAGCTCTAT ACCATGAATA CTGCTGGAAG TGATGGTTTA 250
GGATTACCAA CTCACTGCTG CCATGACCGA 280

178

(2) INFORMATION FOR SEQ ID :330:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :330:

CGTGA AAAAC TTTATGGGG AGAAAGGTCA GCAGCTTCTC TTTCTTTTNT 50
15 CGAAAATNAT AAAACTGCGT ATTCTACTTT ATATTTAATG TAAGGAAGAA 100
AATATACAAG CCCATATTTA CATCGTATTT CTATTAAGAG CAACAATAGT 150
TCATATGTTT ATGTTTGCTA CTATCACAAT NCAACATATG AACACAGATC 200
20 AGCTCTATAC CATGAATACT GCTGGAAGTG ATGGTTTAGG ATTACCAACT 250
CACTGCTGCC ATGACCGA 268

25

(2) INFORMATION FOR SEQ ID :331:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :331:

TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT 50
AGAGTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN 100
40 TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC 150

179

TACCATATGC CCTTAAAAAT

170

(2) INFORMATION FOR SEQ ID :332:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :332:

15 TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT 50
AGAGTTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN 100
TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC 150
20 TACCATATGC CCTTAAAAAT NNGGNNNNNG NNNNGGNTGA ANGGTTCTGT 200
GTTCCAAAAA TMTAAGATT GTT 223

25 (2) INFORMATION FOR SEQ ID :333:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :333:

AGACAATTGG CGGCATCCTC GTAGGCTTCA CTAATCCCA CAAGTTCTTC 50
TGGTTTCATT TCGGTTATTT TTTGCAGCCA ATTCTCTCCA TGTTTGGCAG 100
40 TCACAAGGCT CATGTGCTTC ACCAAGGCAC TC 132

180

(2) INFORMATION FOR SEQ ID :334:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :334:

AAGTTGTTCA TGGNAGGCAT TTATCCTNTC AATAATNCAA ACGAGGCTTC 50
15 TGGGAATAACC AGTGCCCCAT TCCATCAGAG TCTTTGCGCG ACTAAAGCCT 100
CCATNTTTGC CAATTTCAAT TGTTGGGAT TCTAGCACTC CTTACCNGCA 150
GTAATGCCCT TGCTGCAGAC AACAACACCT GGA CTGNGAG ATGGACCAAT 200
20 TCTCAATGGC AATCCAGGGA AAGAGTGATC CTTCT 235

(2) INFORMATION FOR SEQ ID :335:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :335:

35 ATGCCCCGCAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC 50
ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTC AAGTTTCGA 100
CACTGGTAAC CTGTGTATGG TGA CTGAGGT GCTAACCTAG GAAGAATTGG 150
40 GNGATCACCA ACAGGAGAG 169

181

(2) INFORMATION FOR SEQ ID :336:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :336:

ATGCCCCGAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC 50
15 ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTC TCAAGTTCGA 100
CACTGGTAAC CTGTGTATGG TGAAGAGGT GCTAACCTAG GAAGAATTGG 150
GNGATCACCA ACAGGAGAGG CACNCTGNAN TCTTTTGGCN NNG 193

20

(2) INFORMATION FOR SEQ ID :337:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :337:

CAAAAGTCAT CCACAAGTTC TTTGTCTAGG ACTTCTAGCT GCTCAGACCC 50
35 TCAGGGTCTT TGGATTGTTA CCAAAGTCTG TCAAACAGAC CAGTAGTTTA 100
ATACCTGTAC AGAAAAATGT TTCTATTATG CTTCTAGTAT CTAGAAATTG 150
CTTGCTACAG CATGGAGGTG GTTCTGCCTT TCCCTGGCTC CTCACACTCT 200
40 CATCTGCAGG ATTCCAGCT TTGCTCAGTC TTCATGCCCA CCAGAGGCCA 250

182

AAAGGCAAAC TAAAACTGTC ATGCAGTGGT AGGTTTGAAA TNAGCTGCTG 300

CATCATG 307

5 (2) INFORMATION FOR SEQ ID :338:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :338:

AAAAGTCATC CAÇAAGTTCT TTGTCTAGGA CTTCTAGCTG CTCAGACCCT 50

CAGGGTCTTT GGATTGTTAC CAAAGTCTGT CAAACAGACC AGTAGTTTAA 100

20 TACCTGTACA GAAAAATGTT TCTATTATGC TTCTAGTATC TAGAAATTGC 150

TTGCTACAGC ATGGAGGTGG TTCTGCCTTT CCCTGGCTCC TCACACTCTC 200

25 ATCTGCAGGA TTCCCAGCTT TGCTCAGTCT TCATGCCCAC CAGAGGCAAA 250

AAGGCAACT AAAACTGTCA TGCAGTGGTA GGTTTGAAAT NAGCTGCTGC 300

ATCAT 305

30

(2) INFORMATION FOR SEQ ID :339:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :339:

183

AATATAAAGA GGAAATGGCT CNTCACCTTC ATAATACCAA GACCTGCTCA 50

ATTTAAGATG GCCCTTGACA TTGAAATCGT ACCTACAGAA AGCTTGNAAG 100

5 G 101

(2) INFORMATION FOR SEQ ID :340:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :340:

GTCGCAGGAG AAAAAAGTCG TCACGTCATG CGAGTGCGCA GGGGGCGTGG 50

20

AGAGTAGCAG TAGAGCAACA AAGTACATAT AGGACAGTGC AGCGAGGACA 100

AGGACTTCCC GCA 113

25

(2) INFORMATION FOR SEQ ID :341:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :341:

ACACAAATAA CTACATNTAC GCAATATAAT NTTTAAAAAT CCAAAGCAAT 50

ATAAAAGAGC AGAGCTAGGA CTGAACAGAA CATTTTGGTG TATAACCGGC 100

40

AGCTCAAAAT CGCCAGCTGA TTGGAGTAAA ACTGATTCTA AGCGTATTAA 150

184

ATACGATTGA TTGTTTCCAT CACTAAGGGT GCCTATGAGT TTCTGAACCA 200
TTTCTAGGG 209

5 (2) INFORMATION FOR SEQ ID :342:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :342:

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50
TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100
20 GCTTTTAATC TTCATTTTTN NNTTTTGTTA TGGTAGGCTG AGATGCTTTT 150
AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT 200
25 TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC 250
TA 252

(2) INFORMATION FOR SEQ ID :343:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :343:

40

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50

185

TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100
GCTTTTAATC TTCATTTTNN NNTTTTGTNA TGGTAGGCTG AGATGCTTTT 150
5 AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT 200
TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC 250
TACAAAAC 258

10

(2) INFORMATION FOR SEQ ID :344:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :344:

GAAGGAACCA GTGACCAGTC ATCCCCAGAG ATAGATGAAG ACCGGATCCC 50
25 CAACCCACAT TCAAGTCCAC TTTGCAATGT CTCCACGGCA ACGGAAGAAG 100
ATGACAAGGA TCACACCCAC AATGAAAGAG CTCCAGATGA TGGTTGAACA 150
TCACCTGGGG CAACAGCAGC AAGGAGAGGA ACCTGAGGGG CCGCTGAGAG 200
30 CACAGGACCC AGGAGTCCGC CCACCTG 227

(2) INFORMATION FOR SEQ ID :345:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

186

(xi) SEQUENCE DESCRIPTION: SEQ ID :345:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50
5 TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC 100
CTGGCACACT ACTAACTGT AAATGTTTTT AAATCTGAAT CTGTAGAATT 150
CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCA 188
10

(2) INFORMATION FOR SEQ ID :346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :346:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50
25 TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC 100
CTGGCACACT ACTAACTGT AAATGTTTTT AAATCTGAAT CTGTAGAATT 150
CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCATG NCTCTGGATT 200
30 NNCTNNNAGG TTTTAAGATG GAGCATCTGN GNATGTCAGC CCGTCCTATC 250
TAGAAGTGNA AA 262

35

(2) INFORMATION FOR SEQ ID :347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

187

(xi) SEQUENCE DESCRIPTION: SEQ ID :347:

5	CTCTGTTTTT CAAACGCCCA TGTGTGCTAT ACTACAACTC TTCTCGAGTC	50
	TGATCAATTT GCAGTAGACC ATTTTAGTTC TTACGACGTT AATAACAAAC	100
	ACTTCAACAT CANTGCTCCA ATCTGAAGTT CTTGTTGCAT TGTAAAAGA	150
10	AATNTCTAA	159

(2) INFORMATION FOR SEQ ID :348:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 283 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :348:

25	TCGCAGGAGA AGGAAGCTGC ATGCACTTGA AAGGCATGGC CTGTCTCCTC	50
	ACTGAGTGCA AGGTCCATCG ACCAAAGCCC TGTTCTGATC AATAACATCT	100
	ACAATCGCAC CAATTTTCCG GCATGAGGTC CAAAGGAGAC ATAGGCCACC	150
30	CGGCCAACCT CCACGAAGCG CCTGAACACC ATGCGCTTCC CGGGACCCTC	200
	TGGGAGCCGT TCGCNCCTCA GCTTCCCAGC GAGGTGGAGG TCGAGCGGCA	250
	TGGNCGACGC CCCGGAGCCC ACAACAGTAA GAC	283

35

(2) INFORMATION FOR SEQ ID :349:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 169 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID :349:

5 CAGAAAGGAG GCATTGAGCA AAAACTAGGA AAATCTGAAT AACNGTGGA 50
CCTCGCTTGG TTAATATATT TANACTGGTG ACTCATTTTA AAACTTTCCC 100
GGGCGCGATG GCTCATGTCT GCAATCCCAG CACTTGNGAG GCTGAGCGGG 150
10 TGGATCACCC AGGTCAGGA 169

(2) INFORMATION FOR SEQ ID :350:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :350:

25 GAAGNAACCA GTACCAGTCA TCCCCAGAGA TAGATGAAGA CCGGATCCCC 50
AACCACANT TAAGTCCACT TTGCAATGTC TCCACGGCAA CGAAGAAGAT 100
GACAAGGATC ACACCCACAA TGAAAGAGCT CCAGATGATG GNGAACATCA 150
30 CTTGGCAACA NCACAGGAAG GGACC 175

(2) INFORMATION FOR SEQ ID :351:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

189

(xi) SEQUENCE DESCRIPTION: SEQ ID :351:

AAATAAAAAA TAAGNACCCA ACCAATGCTA CAGATAATAA GAGCTCAGTA 50
5 AATGTTGATT GAATCACTAA CAAAGATAAA AGCAGACGAC ACAGTACCTG 100
GCACACTACT AACTGTAAAT' GTTTTAAAT TGAATCTGTA AAATTTGTAA 150
GGTTTTATGA ATATAATATT ATTAATCTATT ATGTCTCTGA ATTTTNNNN 200
10 NAGGCT 206

(2) INFORMATION FOR SEQ ID :352:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :352:

25 AGACATACTG TAGTGTCTAA ATAATATTTG TCNGAAGATA ACAATTATGG 50
GACTTTAAAG CCGACAGTGA AATTAT 76

(2) INFORMATION FOR SEQ ID :353:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :353:

40 ACATTTGGCC CTCAGACTGT AATTTCCATA CTACTNTGAC TGATACTAGA 50

190

.. TGACCTGGCT GCCTAGGGGC TGTGCTGGTC TGATTTTTTG TGAGACAAAA 100
ACCACTCTAA ACCTCCTGGT GCACTGAGGC TGTACACACC GNCAGAACAG 150
5 GGCAC TGCGT TTAAAAGTTT CTGACCAAGT GGTGACAACA GAGGNCAAAC 200
GTAAGGCTGT CTGGATAAGT TGAACCTNGC TGANCGGTAG CACCA 245

(2) INFORMATION FOR SEQ ID :354:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :354:

20

GGAATCTGTG CCACACAGCT GCACACGACT ACTGGCCAAA GGACAGCCTC 50
AGAACATCAT GAGCTGGCGT GACCTCATGA TGNNCCTCAN TGCTGTGGGG 100
25 CTTCTGCTNG AGGCCAGCAG AGGCTCGTAT GACTACCTGT NAGACCTGCT 150
CTTTGGGTTG AGACTTTTCA GNGACAACT 179

(2) INFORMATION FOR SEQ ID :355:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :355:

40

AAGGAACGNA TGACTTTCCA TCCCTGAAC CAAGGCATGT TAGCACTTGC 50

191

TCCAGCATGT TGTCAACATT TCAACAGAAA TCGCACAAAT GCTACTGTGC 100

AAGGTGCAGC CAATTTTNTT GTAAGTGTGA TTTCTTACG 139

5 (2) INFORMATION FOR SEQ ID :356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :356:

TCCAGGAGAA GGAAACTTC CACTTATAAC TGTNTCAGCC TGACTATAAT 50

GAAGAGACTA GCAACACCTC CTGAACACAA GCCTANTGAG CCCAGTCTTT 100

20

(2) INFORMATION FOR SEQ ID :357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :357:

AGAAGGAAAC ACCAAAGAAA CATCCAAGCA ATAAAGTGGG AACTAACCA 50

35 AGATTTGGAC ATTGGAATGT TTACTGTTAT TCTTTAAGAA ACAACTACAA 100

AAAGAAAATG TCAACAAATT TTTCCTAGCT AACTGAG 137

(2) INFORMATION FOR SEQ ID :358:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

192

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :358:

10 AAGGAACAAG TGGGTCATTC TACTAAGGC TGCCTGTCAC TGCAGTCTTG 50
ATCAGCTTGT CAATTGATA CTCAGCTTT TGGTCCAAGG GACGAAGCTT 100
TTCCAAAACC GTTCGAATCT CTACCAGTCT CAAACTGCA TCATGTCCCT 150
15 GAAGAGATCC TCCTGAGGCT TTGTCCAGAA TGAGGTGGGT CAAATNNANG 200
GGNACATGAG CAGCAGCTGN TCTTTAAC 228

(2) INFORMATION FOR SEQ ID :359:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :359:

30

CAGGAGCAAG GAGGCCATTT TGCTGAGCTC TCACAGCTGC TAGAGATGCT 50
CAATGACTCC CAATACAACC CAAAGAGACA AACGCTTGTT TTTTCTGCCA 100
35 CACTCACCCT GGTGCATCAG CTCCTGCTCG AATCCTTCAT AAGAAGCACA 150
CCAAGAAAAT GAATAAAACA GCCAACTCG ACCTTCTTAT GCAGAAAATT 200
GGCATGAGGG GCAAGCCCAA GGTCATTGAC CTCACAAGGA ATGAGGCC 248

40

(2) INFORMATION FOR SEQ ID :360:

193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :360:

10

AGGCACCTGT GGAGCCATCC TCCTTGTTTT AATCGTCCTG CTGCTGCTGC	50
CGTTCCGTGT CGCGTCGCCC ACATGACCCT GAGGTCGCAA TGATGAGTCC	100
TCTCTGGTCA GACACCGCTG GAAATGAATA CCAGGCCTGA CCTCAAGCAA	150
CCATGAACTA GCTATTAAGA AATACANNGG NAGGGCGGCA GCCGGATCGT	200
GNNGGCGTTT NTCTGNGCCG CCCGTCTCAA TCTNTGTTCT GCTTCAGAT	250
GCC	253

20

(2) INFORMATION FOR SEQ ID :361:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :361:

35

GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG	50
GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT	100
CTAAACNGGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA	150
TAAT	154

40

194

(2) INFORMATION FOR SEQ ID :362:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :362:

GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG 50
15 GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT 100
CTAAACNGGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA 150
TAATCCTGNC CACGCCCT 168

20

(2) INFORMATION FOR SEQ ID :363:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :363:

AAGGGATAAA AGGAAGCTTT GNCACCACTC TACCATCAAA NNGGAATTGA 50
35 ACATTCCCAT TAAGGCAGTA AAACAAAAGC CAATAGCAAA CATGNATTTT 100
ATTCAACCAT TGATAGATCT CTGCCGTTAT TCTTCAGTTT CTCTTCTCGT 150
CTCTCTATTT NTTTCTCTGG TTGTCGACCA GCTGACTNTG NCATCGTT 198

40

(2) INFORMATION FOR SEQ ID :364:

195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :364:

10

TTATACAAGT CAAACTTGGG AGGTCATAGT AAGCATACCT ATGCTGAGAG 50
AAAAGCATCA AATCCTCCGC GACACATCTA GTTCATCGTA ACAAAGCAAC 100
TCGTACACTT TCAAGTTTAA A 121

15

(2) INFORMATION FOR SEQ ID :365:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :365:

30

GGTAAGTTGT ATTTGGGCCA GAATTTTAAA GAGCACTATT TCGACATTAA 50
AATGTATTCT TCTCGTATTA ATGCCTACAT CTTCAGAGTT TTCAATGCTT 100
TCTAAAAGTT TCCTCTTTGG AAAGAAGAAA TCTGAAAGAC CTATCATGCC 150
GTTCTTCCTG GCGTCTATAT TTCCTTTAGA GAGGCAAGGT AGGATTCCGT 200
CTCCAAGGGA G 211

35

(2) INFORMATION FOR SEQ ID :366:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs

196

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :366:

CGGCTACAGC ATCACATCCA CTAAATGCAC AGTTGTTGAA GTCACGCCCT 50
10 GCCAGACCTC TACTACCACA TTGTTCCCTC CGGTGACCAG TTTGTCCGTC 100
ACTGTCAGGA GAATGNCCCG TGTCGAATCA TCGATCTCCA TCCGAGCCAA 150
15 AAGTTTTCCA TATGCTGAAA TTACTGAATT GCCCTCGTTT ATAGTATATG 200
ATACAGTGGC CTTCGTTGGA GGCAGATATC AAGCATGGGG ATAAGCAGTT 250
TTCTGGTCCT TAAGGGCTCT CAGCAAATCT CCGTG 285

20

(2) INFORMATION FOR SEQ ID :367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :367:

GACACTGAGG CAGCTACTGA GAAGGGCAGA ACATGTCTCA ATCCATAGAG 50
35 GTCTTGCCAG GCGAACCCAG AGAGACTTGC AGTACGTGAG AAGATGGAGA 100
ACCAAATAAA AGGACTGGAG TCCAGTTCAA ACAAGGAGGG AGTGGTAGT 149

(2) INFORMATION FOR SEQ ID :368:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs

197

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :368:

GGTTCCCGCT CTCACAGCCA TTGCAGTACA TGAGCTCCAT AGAGACAGCG 50
10 CCGGGGCAAG TGAGAGCCGG ACGAGCACTG GCGACTTGTG CCTCGCTGAG 100
GCAATACTAT AATANGCAAG GAACTTTTGA GGCCGAG 137

15

(2) INFORMATION FOR SEQ ID :369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :369:

GCCATCATAA GTTCAAAAGA AAAGAGAAAG TGTTATTTTT CTGTTAGTGA 50
CATGTAGTCC CTTTGTCTA GTAGGAAAAA AGGTGCCTAG AGGTAGTATA 100
30 TAGAGTAAAT ATTGTTTCCTT TGCCTACTCG TGCTTCCAAT GATTAAGGAA 150
ATGTTAAACA NNNGTNAAG TCTGTTTTGT CAATGCGGGA GT 192

35

(2) INFORMATION FOR SEQ ID :370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :370:

5 GAGACTTAAG TAAAACGGCT GCAGGCCAGA TTCGCCCACC AGCTCAGAGA 50
CCACCTTTAT CCATGCTTTG AAGTAGGACT CCTTCCGTCT TCAAAATNTT 100
GAAGACCCTA ACANGCTTTT ATGATGGGGG TCATATCTAT GGTCACGNAT 150
10 ATAGTAGAAA CCAAAGAAT GTAAGTATTT GTNNATGATT TAAAAAT 197

(2) INFORMATION FOR SEQ ID :371:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :371:

GCATCTGNCA GCTGCTGCAG GCTGACAGCC TCCAGACCTG GACAGAATTC 50
25 ATACACTCCC GGAGCTGAAA AAACCGAACA TAAGGGAGTG CACAAGAGCC 100
GGGCTTTGGA GAGG 114

30 (2) INFORMATION FOR SEQ ID :372:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :372:

CTTCTCTAC TCCATCCATT ATCTCCGGGA TTCTCCACA TTCCCTTCAG 50

199

CTCCTAGTTG TTCCACCTTG GCTAACAATT TACCAATCTT TTTTCTATG 100
AACACGTTCT GCCTTTGCTG CTACTTC 127

5 (2) INFORMATION FOR SEQ ID :373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :373:

AAGCGCTCAA TTCGCATCCA CAATGCAACC ACGAACTGAT TTTCTCTTTC 50
TTTTTCAGTT CTCCTTGGTC TGTAACAGGA ATGCCCCCTTA CTCAGTAGCA 100
20 GGCGGACACG GCCATGGGTC AAGACACCCT GCTTCATGGG GAAACCTTGT 150
TTGTCGTTCC CACCACTGAT TCGGACCACA TAACCTTATN NNATCCCGAG 200
25 CGTTAGCAGC AACTTTTGTG GCCATACGCT TCTCATAGAA AGTACGAAGT 250
TTGGCAT 257

(2) INFORMATION FOR SEQ ID :374:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :374:

40

GCATCATCAT TGACATCCCT ATCAATGTCT ACGCTGCTGG CAGAGGACTG 50

200

NCCATTTGGA GCTGAGATGT GTAAGCTGGT GCCTTTAATA CAGAAAGCCT 100
 CCGTGGGAAT CACTGTCTGA GTCTTGTGTC TAGTATTGAC AGATATAGCT 150
 5 TTGTTCTTGG AGTAGAATTA AGGAATTGCG 180

(2) INFORMATION FOR SEQ ID :375:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :375:

GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT 50
 20 TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGNC 100
 TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT 150
 25 TCAACCAAAA TNGATATCAG CAATGTAAAA ATCCCAAAAC ATCTTACTGA 200
 TGCTTACTTC AAGAAGAAGA AGCTGCGGAA GCCCAGACAC CAGGAAGGTG 250
 AGATCTTCGA CACAGAAAAA GAGAAATATG AGATTACGGA GCAGCCAAGA 300
 30 TTGATCAGAA AGCTGTGGAC TTA 323

(2) INFORMATION FOR SEQ ID :376:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

201

(xi) SEQUENCE DESCRIPTION: SEQ ID :376:

5 GGGGAATCCC ACCTCACCCA TTGNGGTGAA ATGCTTTTTT CTAAGAGGTG 50
AAATCACTCG CTGGTGTTA TTTCGGCACA ACCAGAAAAT AGTGNGGGAT 100
ATTGAATTAT GGGAGGCTCT GACTGTCTCG NGTGCAGCTT ACATTACAG 150
ATGGGGGGTA GTTTTTATAT TCTATAAGCG AGCATATTAA ANGCAATATG 200
10 AGTCAGTCCT GCATTTATGT CTT 223

(2) INFORMATION FOR SEQ ID :377:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :377:

25 GGCTCAGGAT CCGGCATCCT TTATGCCTCC ACAGCACCTT GCTCTTTCCC 50
CAGCCAATCA CTTTAGATGC TGAATCGATT TTAACANAT GTTTTGT CAT 100
ATGGCTAATC AAGAGCCAGG TA 122

30

(2) INFORMATION FOR SEQ ID :378:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :378:

202

GGCAGTGCGT GCTTCATCCC TTTATGAAGA ACAGAAAATT ATGACTACTC 50
TACAAGGTGG ATAATACTTC GGTACCTTGC TTGCCACAGC CCTGTTCCTC 100
5 AAAGCTGAAT TGATAAATTT CTCTTTGACT TCCAAGACCT AGCAGTTATA 150
AGGCGCCTTG AATAAAGTTT GTGCCTGAAA ATGTGGAGCA ATGCT 195

(2) INFORMATION FOR SEQ ID :379:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :379:

20

GTAGCCCTGA GGTATCCTG CAAAGNGCGT ATCAAAAAAN ACGAAGTTAG 50
GGTGACAAAG TTTGACAGTG ATGTTTACAA GTCAAACCTG GAAGGTTATA 100
25 GTAAGCATAC CTANGCTGAG AGAAAAGCAT CAAANCTNNG GNACATANTN 150
GGTTTNTNGN AACAAAGCAA CTTGTAATTT AAGNTTAAAC NGAGCATCAT 200
ATANNNNNNGG 210

30

(2) INFORMATION FOR SEQ ID :380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :380:

203

CTGGCTCACC TGGACAACT CAAGGGCACC TTTGCCACAC TGAGTGAGCT 50
GCACTGTGAC AAGCTGCACG TGGATCCTGA GAACTTCAGG CTCCTGGGCA 100
5 ACGTGCTGGT CTGTGTGCTG GCCCATCACT TTGGCAAAGA ATTCACCCCA 150
CCGTGCAGGC TGCCTATCAG AAAGTGGTGG CTGGTGTGGC TAATGCCCTG 200
GCCCACAAAGT ATCACTAAGC TCGCTTTCTT GCTGTTCA 238

10

(2) INFORMATION FOR SEQ ID :381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :381:

GTCCTATGGC ATGAATGTTT GCAACCAACC CAGGAAAAGC CTAAAGGAA 50
25 ATAGCTGTTC ACATAGGAGA CCGTGACAAT GCTGTACGCA ATGCTGCACT 100
CAACACCAAG CAACGATGCA CAATGTACAT GAGGATCAGG TGTTCAAAC 150
GATTGGAAAT CTTTTTGAAA AGGATATGAG CATGCTCGAG GAGAGGATTA 200
30 AGCGTCAGCA AAGAGACCCT CTCTGCACCA ATAAACAGG TGGAAGAAAA 250
CCTAGCNCGC ACAGAACATA AGCTC 275

35

(2) INFORMATION FOR SEQ ID :382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :382:

5 AAGCAGAGTA CGCACGTCAG GCCCTTCCAC GCCCACCCEA AACTTTTAAA 50
CNTACTGGGC GATGGGGCCG TTTNGCTGGC AGTTCAAGAT AAAACA 96

(2) INFORMATION FOR SEQ ID :383:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :383:

20 GGACTTGATG GCTTCTTTCA AAGTCATAGA CTTGTGGTAA ACTTCTTGCA 50
AGGAGCTCTG GGCACCCTCT GAAGCAGAGC CAATTGCTCG AGCATCACAC 100
TGTACAAAGG TCCAGATGGG TTCATATGAA ACAGCTGGAG TCCTTTTCAT 150
25 CAATNCNAAT NGANNGGTTA CTCCAAAGGG ACGAGACATG CACCTG 196

(2) INFORMATION FOR SEQ ID :384:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :384:

40 AAGGAGGCCT TTGAGTCCCA TCCTCTGCCA CGCAGAGAGG CAGGCCTGGC 50
ATTTCAGCCT CACTTTGTGT AGGTCACTTT TCGGTCTGTG TTGTAGCTCA 100

205

CCAACCAACA GTCAAACCCC AGCGTGGTAG CACGAGGTCC AGAACCTCTG 150
CTTAGTGGGC CCGTATAATA AACGCAACCT GACCCAATTN NGGTTTCTTT 200
5 CCCCAT 206

(2) INFORMATION FOR SEQ ID :385:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :385:

GAATGCTTGG GATCATCCAG GTGNCTCTAT TTATAGGCAC CTGTGTTTAC 50
20 CAGCAGTCTC TCTATTAGAA TGCTTGGTGT GCCAATGTTT CTTGAATTAG 100
AAGCCTGGGG NCACCTAGGT GTTCTATTA TAAA 134

25 (2) INFORMATION FOR SEQ ID :386:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :386:

CAAGGCCTTC CTGCACTGGT ACACGGCGAG GGCATGGACG AGAGGAGTTC 50
ACCGAGGCCG AGAGCAACAT GAACGACCTG GTGTCCGAGT ACCAGCAGTA 100
40 CCAGGACGCC ACGCCGACGA ACAAGGGGAG TTCNGAGGAG GAGGAGGCCA 150

GGACGAGGCG T

(2) INFORMATION FOR SEQ ID :387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :387:

GGTGAGCCTC CGCCATCCAG CAAAC TGTGC TGAC CGCAGCTGTG 50
CCGTGGCAG ATGGCGAGGA AGCCAGCCCC AAGGACAC TGAAAACACA 100
ACCAGTCAAT GCCGTGTGGT TTTGTTTGAA TATAAATNGC TGAAAGTGT 150
GTTTTTTNAG GCAGTAATNT 170

(2) INFORMATION FOR SEQ ID :388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :388:

TCCATCTGAC ATCGCATTTC CATAGAAATG GCCAAGAAA GAAGTCCTG 50
GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA 100
GCCCAATACA AAATACACAG AAAAAGCAAT TATTAAAAAC GGCTTCGGTT 150
TCTTTTTTCT CTTTAATNNC CTACAATNGC TTTACATATT CGTGTGCAGC 200

207

ACCTACTTCT TTATGCCGTG AACTGAAATC TAAGATTTC AACTGAAATC 250

(2) INFORMATION FOR SEQ ID :389:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :389:

15 GCCATCTCCC CGCCACCCNC TCGTCCCCTT CTTNTCNNGC CACCCTTCCT 50

CNCTCNTCCG TTTTNGCTCC ACTCCACTCC TCCNTTTTNA GTACCCTCCT 100

CNTTTATNTA GAGTTACTGA GAGCCGACCT GACGTCTCCA ACATNCCGTN 150

20 TCTTATATCT CATCNCGGTT NTNGANGAAT GNAGTNAGGG TTTCCGGGAG 200

AGACCNAACT TGCTCTAGCC CTTTCCAGCC GCTGTTGTTA AACTGACCTC 250

25 GTAGGGCNTG AGGGAGGT 268

(2) INFORMATION FOR SEQ ID :390:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :390:

GTCAGAGGCA GCCCATCCAG CACGTGCTAG GTGTTCCCAT ACGCACAGGA 50

40 GAGGCGAGCT AGCCAGCCAA GGCGGGCAGG CGGGGAGGCC CTCTAGCTGT 100

208

TTGCCTCACC TGTGGGGCCC CAGCAGGGAG GAGTCACCAG CCTAGAGGGG 150

CCAGGTATAC ACCTTANAGA GGATGAC 177

5 (2) INFORMATION FOR SEQ ID :391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :391:

GCTCCACTTC CCACATAANA CNAGACCTCT CACAAAAGAG TTCACTGATA 50

TGTGAATGCA GCTTTCTCCC CATGGTAGCC AGGACAGGGT GCACATTAAG 100

20 GCAACCCCAA AACACCTCT TNCTGNCTGC CTCTGCAA 139

(2) INFORMATION FOR SEQ ID :392:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :392:

35 GAGGAGCTGC CCTCAAGGTC GTGCGTCTGA AGCCTACAAG AAAGTTTGCC 50

TATCTGGGGC GCCTGGCTCA CGAGGTGGC TGAAGTACC AGGCAGTGAC 100

AGCCACCCTG GAGGAGAAGA GGAAAGAGAA AGCCAAGATC CACTACCGGA 150

40 AGAAGAAGCA GCTCATGAGG CTACGGAAAC AGGCCGAGAA GAACGGGAG 200

209

AAGAAAATTG ACAAATAATA GAGGTCCTCA AGCCCACGGA CTCCTGGTCT 250

GAGCCCAAT 259

5 (2) INFORMATION FOR SEQ ID :393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :393:

AAAGATCATC AGTTTGAAG GTACTGGTCC AATTATCTA GGAAGTATCT 50

CTTGGAGTTT CAGAAATGCT AGCTTGACA ACTGAAAAGT CACATCACAG 100

20 CTGGCATTCT GGGGGCTACC AAAACACCCC TCNNGGAGTA GAAGCTGCTG 150

GAAGGCAGGC CTGAGCCATT CACCACGGAC AGGAAGAGC 189

25 (2) INFORMATION FOR SEQ ID :394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :394:

AGAAGGGGAG GTCGAAGAAA TGTGGCTGAT CATAAGAAAG GAGCAAAGAA 50

AGCTAGAATT GAAGAANNNN GAAAGAAACA GAGGACAAAA AACAGA 97

40

(2) INFORMATION FOR SEQ ID :395:

210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :395:

10

AAGAGGGGCT AAGACCCAAG TCATCCTCCA CTTTCGTTTT GTTATATTTT 50
GCTTAGAATT GCCTCTTCTT CTCCACTTCA GAACTGCCTC AAAATTGACC 100
CCCTTGACTG ATTTATTGTC GTCAAAGCA TGTTCTCTA TCTTTNNNN 150
TCAGACGATC CGCTGCCTTT CTACATCTGA GAATCTTGTC AAGCATGGAT 200
AAACTTGNTT TTATGTTGCA TATTTTNACG GCTTCAACTT GAGT 244

20

(2) INFORMATION FOR SEQ ID :396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :396:

TAATATCGCC ATGTAATGGT ATACATTGTA AGGCTTATGT CACTAAAGAT 50
TTTTATTCTG ATCTTTCCAT AATAAAGGTC ATATGATACT GTATAGACAA 100
GCTTTGCAGT GAAGTATAGT AGCAATAATT TTCGTACCTG ATCAAGTTTA 150
TTGCAGCCTT TCTTTTCCGT TTCTTTTNTG AAGGG 185

40

(2) INFORMATION FOR SEQ ID :397:

211

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :397:

GGACACATCC ACCCAGTGAA CTGGACTGTG GCCATGACCC AGGGTATCAG 50
CTCCAAACTC TGCCAGGGCT GAGAGACACA TGAAGGAAGA TGATGGGAGG 100
AAAAGCCCAG GAGAAGTCCA CCAGGGACCA GCCCAGCCTG TATACTTGCC 150
ACTTACCACC AGGACTCCTT GNTCTGCTCT GGCAAGAGAC TCTTGTCTGA 200
ACACTGCTTA TCTGACCC 218

(2) INFORMATION FOR SEQ ID :398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :398:

GGAAGCAAAA AAACAAACT AAGCTCGAAT TTGCTTCCAA ACCTGTAGAT 50
TGCATCTAAC CANGTGTCCT TATGCACCTC AGAGTACTGG AATACGAACC 100
CAGCGAGACC TTGTCCCCTC CCATTTTGCT GNACTTTTGT TGGTGAAAAT 150
GAGAATGAGT TNATCCCTAC NTACTTAGTT TAATGCATT GACCCAGAA 200
AACCCAGTA CCTTTNNACA ATGACCCAAC CANTACCTAC CATCGGCCAG 250

212

(2) INFORMATION FOR SEQ ID :399:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :399:

TCACTTGATT CATCCGTCGC GGGATTGGG AGCACTAGCA ACATAATCAA 50
15 CACACTCCTA CAATCTTAGG CTTACATGT GCTGATGATG ATGAAACCAA 100
CTCTGCCCCA ATCATCTCCC CTTCTNTTAG GGTCTTACTA CATATCGCAA 150
CAGAAGATAA TATTGAGGTG AAGAGGGTAA CATGAAGTTT GGCCTACCC 200
20 TGAAGAACTG TAGGCATCTC TTGGAATGTG CTAAGGAACT TGATGTCCAA 250
ATAATGAGAT TAAATTTATG TTTTCGAGT 278

25 (2) INFORMATION FOR SEQ ID :400:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :400:

GGCCAAACTC ACAGGAGCCT AGGCACAGAG CACTGAACAC TGGCTCTGCA 50
GCGGGAAGGA ATTAGAGCCT TCTGCTTTTG CACCTGCTTT GAGTTAGGAA 100
40 GCAAGCTCTC TTCCTTGCCA GACTTCCCTT TGGGGCAGGA CACTTTTTTA 150

213

TACNCTGAGG CAAGGCAAAC AGTCATAGAA CAGTTATTAA ACAATANAAA 200
ATGTGTT 207

5 (2) INFORMATION FOR SEQ ID :401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :401:

GAGGCATGGC CACATTCCAA GAAATGGAAT AAGGAGTGGG ACAGCAGGCA 50
GGGGGCCACC CTGGGGCCTG GGCCTTTTAA TCTAAGGACT GGGGAGAACC 100
20 AAGGGACCTT AGAGGTCCTC CAGTCCTCCC CATATNNAAA GAGGGAGAAC 150
AAGCCTGGAG AGGAGGCTAC CTTAAGACCC TAAGAAGAAT TTAGCAATCG 200
25 NTTCTCCAAA GATAGCC 217

(2) INFORMATION FOR SEQ ID :402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :402:

TTTACAATAG ATTTACCTT CANTTTAGTC AGAGTTGTTG ATTCAAGACT 50
40 CTTCCACAC TCGCACATCG AACATTTTT GTGCCAGGGC TTTCCAGCTC 100

214

CAATTATCTT CTCGACAGCA TATACAGAAT CCCCACATCT GGAACACTTC 150
TCAGCACCTC CATANNTTGA GCAAATTTAG AAGTGTTTGG ATTTGTTGTA 200
5 GGCCTGTGAG GCTGAACACT CTCTG 225

(2) INFORMATION FOR SEQ ID :403:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :403:

AGAAGGGGCA TACTCGCTGG AGACCTGGTG CCTCTATCCA CTGNACGCTG 50
20 ACTGNGGCTT CCACTGCGCC CGTGACNTT ATCGAAGCTA CAGAT 95

(2) INFORMATION FOR SEQ ID :404:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :404:

35 AGGAAAAATT GACATTACTT GTTAGAAGAG CAACTCTGAA AGAAAACAAG 50
CAAATTCCAA AACAGAAAAG ATTCACAATN NAAAGGTGCA TACATTAAAG 100
GGCCCACTG TGTAATACTG TGCCAACTTA TGCGAGTCTC ATTGTTTCAGG 150
40 ATGAAATGTG AGATTGTAGT TTGAATGCTA TAAGCAGGTT CCAAGATACC 200

215

CCAAATGACT GTAAGCCAGA CTNGAAGCAT GTCAAAAAG

239

(2) INFORMATION FOR SEQ ID :405:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :405:

15 GGCTATTATT CTAAGTGAAG TAACTCAGGA ATGGAAAACC AAACGTTGTA 50
TGTTCCTCACT GATCATTGAG AGCTAAGCTA TGAGGACTCA AAGGCATAAG 100
AATGATACAA TAGACTTTGG GACTTGGGAG GAAGAGCGGG AGTGGGGCGA 150
20 GGGATAAAAG ACTACAAATA TGTGCAGTGT TTACTGCTC 189

(2) INFORMATION FOR SEQ ID :406:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :406:

35 CACCATCCTC CAAGTAAATC CCCCTTAGG AAAGTAAGGG AAAAGACCCC 50
TTATAGCCCT GAGCTCCCCC TTGGA 75

(2) INFORMATION FOR SEQ ID :407:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 base pairs

216

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :407:

10	TATTCATCCA GCAGTGTTC TCAGCTCCTA CCTCTGTGCC AGGGCAGCAT	50
	TTTCATATCT AAGATCAATT CCCTCTTTTA GCACAGCCTG GGGAGGGNGT	100
	CATTGTTCTC CTCGTCCATC AGATCTCAGA GGCTCAGAGA CTGCAAGCTG	150
15	CTTGCCCAAG TCACACAGCT AGTGAAGCCA GAGCAGTTTC	190

(2) INFORMATION FOR SEQ ID :408:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 194 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :408:

30	GAAGACATGG CGCCCTAACA CTCGAGACC TGCTGNTAAA TTAAAAGCTA	50
	TTTTTCATTA AACCACCATT TCCTCCACCT ATTGGAGTCA AATATGAAAG	100
	CTGTCGATGA AGCCTGNCTG GCTGCACAAG TTNGACTGNG TCTGAATAAG	150
35	CACTTTCATC ATGGACTAAG AATCCTTGGT GTGGNCNTGA TCTT	194

(2) INFORMATION FOR SEQ ID :409:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|---------------------------|
| 40 | (A) LENGTH: 97 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |

217

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :409:

GCAGCACAAG AGTCATCCAT GGATACAGTT CCAATCATT TAACCACTTC 50

TAAACAAGA TCATCTTCTG CAGCACCTGG TTTAGTTTA TCCTTGA 97

10

(2) INFORMATION FOR SEQ ID :410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :410:

TTTGAGCTCC TGGACCCTTC TTGCCTACA CTGGCCTTC TCTCGGAGGG 50

25

ACAAGGAAGC TGGCCTCCCT TTACTCTACC NTTNNTNTG GTCCAGGGCC 100

AGCTCTTCCG AGGCTCCAGC CTGCTTTTCG CCGGTGTCAT CAGATCATGC 150

TTTGC 155

30

(2) INFORMATION FOR SEQ ID :411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :411:

218

5 AACGAAGNGT TCCTGAATAC CACAGCCTGC TGGGAAATGA CTAGGCGGTA 50
AGGTTCTGCC ATGCCTGTGA CCCACCATGG ACATACTGGA CCTTAATTCC 100
TCTGCTTCTG TGCTCCCTCC TGAGAACCCT TTATGAGCCT GATTCCTCAG 150
TCTCACCAGA ATTCTGGATC ACCCAAGAGG AAAAGACTGC CAGTTCTAGA 200
TTCCTCTATA GGGAGACCTG GATTGTTGAC CAGGTGAGAA GCCAATGGT 249

10

(2) INFORMATION FOR SEQ ID :412:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :412:

AGAAGGAGAC AAAACACCTC CTCTGTAATA GTACCTCGAA TGGATTCAGC 50
25 TTTACTCCTC TATAACTCAT CTTACACCN GCATATTTAA ACAAACTAAC 100
AAAATGAAAT ACTAATAGTA AAAAGGCTGA CCCATGTGGC TTT 143

30

(2) INFORMATION FOR SEQ ID :413:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :413:

GGGTCCCCC ATTACGTAC TCCATCACA AGTACAGGCG GTCCATGGTC 50

219

100 TGGAAGCAGG AGTGGAGCTG TCAGGAAGGG CGGCTTCCCG GGCAGGCCAA
150 CACCCACTTC TCCACCATAG TGCCTCCAC GTCATCATCT GATCACAACG
5 TCCTTCTTCA GGATCTTCAC AGCATAGAGC TCATCTGTGC CTTTCGTTCT 200
GAAAGCATGA CCTTGCCAAA GCTGCCTTTC CCCAGCACCA TTAGGAAGTT 250
AAAATC 256

10

(2) INFORMATION FOR SEQ ID :414:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :414:

TCGCAAAAGA AGNGTACCAT AACTCCTATT TCNAATGGCT GATTGTAGTA 50
25 GCACTGGAAG TTTATCAAAA CCCAGGTGTA AATATGC 87

(2) INFORMATION FOR SEQ ID :415:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :415:

AGAGGGGGAC CAATCTAACC ATCGCTCTTC CAGTCCTACC AGCACACTCT 50
40 TGCAGCGCCA TNCCACTCCC TGAGCTCAGG ATCCTAGCCC GCCCCCCCCG 100

220

GGATGCTAGT NNNCTCCACC CTNCCCACCT GTCATACCTG TGTANTACAC 150

ACCCACCCGT ATCACGCAGG ACATGAACCA GCACCACTAA GGCCCCGGNG 200

5 CAGTGTTCTG NNNTTCTTCT CTANCTGTCT GCCCTGAGTC CCGGACC 247

(2) INFORMATION FOR SEQ ID :416:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :416:

TCTAGCACAC AGCTGCGCTC AAAAAACTG CGCGACTTGT TAGAACTAAT 50

20

TGAGTGGAGC CTGCAGGTGA GGGGAGGGAG GGGCTGCAGG TCAGGTAAGA 100

TCTGGAAGAC AACGCACACT TGAAGGGCAG GGGACTCTAA GCAGGGATTT 150

25

ACATTGAAAG GA 162

(2) INFORMATION FOR SEQ ID :417:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :417:

CAGAAGAAGG AGAACTCATG ATTCCAGAGA GCTTTGGGGC TTATTTTAA 50

40

GTACTTAGCA AAATATTTGT TTTNCGTGAT TTAGCTTGTC ATTAAACNAA 100

221

GAGCTACTG

109

(2) INFORMATION FOR SEQ ID :418:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :418:

15 GGATGTAAAT TATATGTTGT TTAAATTTT CCAGCATCTG AAAACCTTAT 50
CTGCTAGACA ATGCAAGATT CACACAGAGT TATCTGGGAT TCTGATTTT 100
TAAATAGTAC ATATCATTAA ACCATTCNTT CTAAANGTAA GAAGAGCAGA 150
20 AAAAATCTTA TAAGATTATC AGATTTTCCT AATGACACAG AAATGNAAGA 200
AA 202

25 (2) INFORMATION FOR SEQ ID :419:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :419:

TAGCAAATGT GGATTACAAG CAAATACAAC AAGTCGTGCC CCTCCAACCC 50
ACCACAACT TCTAAACGCC ACTCAGCAGA TGCATAGGAT TCGTTACACG 100
40 CAACGATTGA AATAAAAATA AAAGCTNCAA ATGCAATACC CANACTAGCC 150

222

TA

152

(2) INFORMATION FOR SEQ ID :420:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :420:

15 CAGCCCTACA CTCGCCCCG CCGATGGCCTC TGTCTCCGAG CTCGCCTGCA 50
TCTACTCGGC CCTCATTCTG CACACGATGA GGTGACAGTC ACGAAGGATA 100
AGATCAATGC CCTCATTAAG GCAGCCGGTG TAAATGTTGA GCCTTTTGG 150
20 CCTGGCTTGT TTGCAAAGGC CCTGGCCAAC GTCAACATTG GGAGCCTCAT 200
CTGCAATGTA GGGGCCGG 218

25 (2) INFORMATION FOR SEQ ID :421:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :421:

GATGCCAATG TTTCATCCAC CGGCTGCACA GGCACAACT CCCCCACCCA 50
GGACGACTGT GATGAGGTGG CCCTCCCTGT CAACCCTGGT CCCTGGAGTC 100
40 CCCAGCACCT GGGGCCCTGA CGGTCTCGAT GTCACAGGCG CTTACTGTGC 150

223

TGCTGGCTGT CCTATGCCAG CCTCACCCAT GTGGGGACCA CGNAAGGCAC 200
ACTCCCTCAC CCCGGTGCCG GGCCGTGCGA TCCCCCA 237

5 (2) INFORMATION FOR SEQ ID :422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :422:

AGGNGTAATA AATACTGCAT CCTTCCACA ACATAGCAGG AATCTTATAG 50
GGAAATCCAT ATAGTTTCTG AACATGTATT NATATACTAA GTCTATATTG 100
20 TTTCTTTACG AAGTGTAAT AAGTGCTGCA CCATACTGTA AACAAAATC 150
GAATATTGAC TAAATAAAAT CAAAAGTTCA TCTTGTAGTC ATGTCTTTCT 200
25 CC 202

(2) INFORMATION FOR SEQ ID :423:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :423:

GGGACACCAT TACCATCCAT TGACATCGCA TTTCCATAGA AATGCCAAAG 50
40 AAAGAAGTCC TGGGGTTTTT CATAGAAAGC TCAAAAAGTT CAACCTTTGA 100

224

TGCTATCCCC CAGCCCAATA CAAAATACAC AAAAAAGCAA TTATCAAAT 150
 ACTGACTTCG GTTCTTTTT CTCTTCAAAT NCCTATAATN GCTTTACATA 200
 5 TTCGTATCAG CACCTA 216

(2) INFORMATION FOR SEQ ID :424:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :424:

CGACGAAGGG AGTACTCGCG CTTTGTCTCC CTATCCACAC TTGAGCAAAT 50
 20 GCTCGCTGGT CTACTGCCAA AACCCATTC ACCAACCATA TGTCCCTCGC 100
 CCATACCCCC TCTCCCTCTC AAACCCTGGG GACAAATTCA AGGACCCAGG 150
 25 GGTGCCCTTT TAAAAAA 168

(2) INFORMATION FOR SEQ ID :425:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :425:

TCGCAGGAGA AGGAGTCGCT TACTATGCAT CCAAAGGCTA CCGTGGTTAC 50
 40 TCCTATATGA CATTCCAGAT TTTGATGACT AGCACCCACC CCACAGCTGA 100

225

GAGGAGTCAC AGTGGAAGTT CCCAGCTTTA AGATATCTAG CAGAACTAT 150
AGCTGAGGAC TAAGGAATTC TGCAGCTTGC AGATGTTTAA GAAAATAATG 200
5 GCCAGATTTT TTGGTCCTTC CCAAAGATGT TAAGTGAACC TACAGTTAGC 250
TAATTAGG 258

(2) INFORMATION FOR SEQ ID :426:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :426:

20

TCCACATCAT CTCCAAAGCC CATAGGCCGA GAAATGGCAT CTGAGATCTG 50
CTGGGCCACC TCCTGTTGTT CCGTATGTCA GTCATCAGTT CATCTACCTN 100
25 GTCAATGTCC ATGTCCTGGT AGGCCTTCTT CATGCTTTGN CAGCAAGCTC 150
CATGCACGAA GGAATTCTGC ATTGGTAGTG GCATTCTCAA TAGCCTCACG 200
CTGAAACTCC AGGGTGGATA ATGCCCCGTC AATTGTGCC AGCTGCTGTT 250
30 CGAATNNTTT TCTTCTCGT AAAGC 275

(2) INFORMATION FOR SEQ ID :427:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

226

(xi) SEQUENCE DESCRIPTION: SEQ ID :427:

CTCTGTGCCT CGCTGAGGAA AAATAACTAA AATGGCAAAG AAGATCCTAA 50
5 GAAGCCGAGA GGCAAAATGT CATCATATGC ATTTTNTGGC AAAGTGTCCG 100
GAGGAGCATA AGAAGAAGCA CCAGATGCTT AAGTCAACTN TAAGAGTTTT 150
CTAAGAGTGC TC 162

10

(2) INFORMATION FOR SEQ ID :428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :428:

ATGCAGAAAA GGAGTCGTGA GCGTAACACC CTCGCTGCTG GTCATAAAAC 50
25 CCATAGTTCC TGAAGTCATC AAAGAACTTA ACTTCCTGAC GCCAGATATC 100
TGCCATGCGC GAAGGGNTGA TACCACTCAG GATTATGAAT TTTGTTTAAA 150
GTCGNGTTTA CAATGATTG NCCTGGACTG AAATTCANGC TGCCTTAAGG 200
30 TGCTGATGAT ATTGAGAAGT 220

(2) INFORMATION FOR SEQ ID :429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

227

(xi) SEQUENCE DESCRIPTION: SEQ ID :429:

5 GACTCATCTT GCCCAAGAAG AGCCAGGATA TGAGAAGATG GGAGAGGGAA 50
GGGGAGGTGT GAAACGTGCT GGTGCTTCCT GTCCTCATGG TGTGATGGCT 100
GCCCAGGCTG CTCCTTCGAG GCAGGACAGG ATTCCCATGG GAGATATGAG 150
GACCATGGTG ATTTCCAGGA CCAGTTATGT CCAGA 185

10

(2) INFORMATION FOR SEQ ID :430:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :430:

GGGATGCCCT GACCTGATGG CCCTTGACCA ACATGGTGCT GGAGGAGCAC 50
25 TACCTGGTCG TGGGAGTAGT GGTCATCGTG GACCCAGGGG TGATCCCTAT 100
CAACTCTTGG GGTGAGAAGC AGCGCATGCA CCTGCGGGAC GCTTCCTGGC 150
TGACCAGCTG GACCCCATCT AGTCGCCTAC AACAGCGAGC CAGCACACCG 200
30 GCCCAGGTGC CGGAGATGAA TGAGCCCCAG CAGTCCAAGG TGTGATGTGG 250
GAAGACACCG CAGAGCTCAC TTACCAA 277

35

(2) INFORMATION FOR SEQ ID :431:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

228

(xi) SEQUENCE DESCRIPTION: SEQ ID :431:

5 AAAGTGGCT TGGGCATCCT GCCAGCCTGC CATGTCTTCA TGGCTGGTC 50
GAAGGCAGCC NGGACTATGG CCAGGAGGCG AATGTAGTCA CTCAGGAGCT 100
CAGCAAGGAG GAAGAAGTCA TTGTT 125

10 (2) INFORMATION FOR SEQ ID :432:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :432:

GCCTAACTGT CAAAGCACAG AAACTTAAC AAAGGGTGGG ACTCGCCATT 50
TCGAAATAGC ACATTTTGTAG CAATAGGCTC TCTACACTAG AGAGCCAGTA 100
25 GACTGATATT CTTTAATGCC AGTTTCCTAG TTAATCGTAA AGATAGACAC 150
AATCCCCCCC TTTATAAAAG CTTCTGTCGT TTCACATAAT GACTTTAACT 200
30 ANAANGGAAA TGGGGCAGGA CA 222

(2) INFORMATION FOR SEQ ID :433:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :433:

229

CCATGNCGGC CCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT 50
 CGATTCCTG GTGCTTGGT TGGTAGCTT AAGCTGGGAT TCGAGGGTCC 100
 5 CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT 150
 TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAAGTGT TGGTNTAACT 200
 NGNCGTTTCC TCT 213

10

(2) INFORMATION FOR SEQ ID :434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :434:

CCATGNCGGC CCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT 50
 25 CGATTCCTG GTGCTTGGT TGGTAGCTT AAGCTGGGAT TCGAGGGTCC 100
 CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT 150
 TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAAGTGT TGGTNTAACT 200
 30 NGNCGTTTCC TCTGCCGGTG T 221

(2) INFORMATION FOR SEQ ID :435:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

230

(xi) SEQUENCE DESCRIPTION: SEQ ID :435:

ACACTTGATA CTATGCATCA AAGGACGTGG AGAACTAGAG CGGGCTACAT 50
5 TAGTATATTT TCGTTGTCAG 70

(2) INFORMATION FOR SEQ ID :436:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :436:

AGTACGCAAT GCTTTCTTAC AGTAAGCAAG AGCTCCTCTG TAATCCTTCT 50
20 CGTTGAAGGA AATGCAAGCT TTACCAAGAA GGGCTGGAAT ATTATTCGGA 100
GACTGATTGA GTACAAAATG AACTGTGCG TCAGCTTGAT CCATTTTGTC 150
25 ACCCTCAAGT AGG 163

(2) INFORMATION FOR SEQ ID :437:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :437:

TGTGGCTGAT CATAAGAAAG GAGCAAAGAA AGCTAGAATT GAAGAAGATA 50
40 AGAAGAAACA GAGGACAAAA AACAGACGT TAAGGAAGAA GATAAATCCA 100

231

AGGACAACAG TGGCGAAAAA ACAGATACCA AAGGAACCAA ATCAGAACAG 150
CTCAGCAACC CCTGAATTTG 170

5 (2) INFORMATION FOR SEQ ID :438:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :438:

AGAACTACAG AAACCTGGCC TCCCTGAGTT TATCCTATGG GGGGCACAGG 50
AAAGAGCCCT GGACCATAGA AACCAAGTAC GAGTAGCAAG AAAACCAAAA 100
20 GGGTGGGAAT GGATCAAAGG TGTGAAAACA GATCTGTCTC GTAAGTGTGT 150
AATCAAGGAA CTAGCACCAC AACAGGAAGA TAACCCA 187

25 (2) INFORMATION FOR SEQ ID :439:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :439:

AAAAGCAACC AGGTTCGAGA AACAATAGTG TATGTGTTCC TATAGGTATG 50
AGTTATTCAN TGTAGATTCG TTTTCTGCA ATCCTCTGCC GAAATGATNT 100
40 ACACTTACAA TGNNGAATGC CATAGGACAC TACAATCTGA ATCAAAACAG 150

232

TCGCGTCTGA AATGNTNGTG TGGTAGACCA CCCCATTCA AGCCTTCATA 200

CTTCGTAAAA ATGCAAATGT TGAAGATCGN NTCT 234

5 (2) INFORMATION FOR SEQ ID :440:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :440:

GGACCAGGAA CCTAACTGAG ATAAGTTCAG CTTTCCAGTT GACACCAAGT 50

CATCTAGTCT TCCCGGAGTA GATATAGTTG AGGTACTCCA TTCCCCAAA 100

20 CAGAGAGCTG ATCCCGGGCT GCAACACCTC CAATAGTCGA AGCTCCCTTA 150

ATNAAGGATA TCAATGTATT TCTTAAACGC TTGATGTCGT TCAAAGTCTG 200

25 TTC 203

(2) INFORMATION FOR SEQ ID :441:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :441:

GTGATGCACC TGACATCCCC TCACAGGCTC TTGGAGAACT GTAGTGCAAC 50

40 TCACTTAACC GCAATGCTGA GAGCAGAATT CTGGAGTATG ATCCAGGGGA 100

233

ACGTTTCCCC ACACCACCCG AGCTACTTTA CCAGCGATCA TGATTGTGAT 150
GGAATAGGCT TATTAAGTTA CACATTTAAA AAGTCATTAG AACATCTCGT 200
5 TCTTGCACAC TAGTGTAGAA AGGTCTTCCA AAGATAAAAG GTGTAGGCCT 250
GGTT 254

(2) INFORMATION FOR SEQ ID :442:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :442:

20

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG 50
CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG 100
25 CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGC 147

(2) INFORMATION FOR SEQ ID :443:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :443:

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG 50
40 CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG 100

234

CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGCTNC 150
TCCGNGNGAG ACGCAGTGGA CTNCGATGNT TAGCNCTAGT NNCCCGCT 198

5 (2) INFORMATION FOR SEQ ID :444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :444:

ATACTACGCT AGGAGAACAA TGTCCTACA TATTATGGGT AGTGAGACAT 50
TATCTGTATA CAGGGACTGT GATTATTTAA AATATGCAGA ACTTATTTC 100
20 TCTGTGCTTT AGAAATAACT GTATACAGTG TTATAAGTGA AAGAACTCAA 150
AATAACTAAT ACCAAATATA CACCTATGTA TTAGAATTCA AAAAGCTGCT 200
25 TTCTGTGA 208

(2) INFORMATION FOR SEQ ID :445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :445:

AGCACATTTC ACTACGGGNT ATGTGCATTC TGGGCTTAGT AATGTCAAAT 50
40 CACTCTTCTC TCCAGCTTGG CCATTCTCA TTCCTTGCGG GCCTGCCCTG 100

235

TAGACCACAG GCTAATGGAA TGTCCCGGTC TGNGTCATCA NATTCTGTAA 150

CCTGNAGCCC CCGCTGAG 168

5 (2) INFORMATION FOR SEQ ID :446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :446:

AGGCAGAAGG GACGCTACTG ACTTAAGCCA AACCCCTGATT GGTGGATAAA 50

GTATTCAGTT GTTCCATTCA TGCCTATCCT TTNTACAGCT CTCGCGACTA 100

20 TAACAAACAA CTGATAAAAT AGCATCAGTC CCTCCACCAG GTTGCCCTCA 150

AGGAAGCCAT GTTTGTGACG ATCCGACCAG TCCCTGACGA TCTCTCTAGA 200

25 CCACCCTGAC CTCGCCGAGA GTGCTGAAGG AGCTATCTAA CCA 243

(2) INFORMATION FOR SEQ ID :447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :447:

CAGTCAGGGT CACAGAACAG TATTCAAAAT GATTGCCCAC CTGTTT TAGA 50

40 AATCTAAAT NNTAAGTAAC TAAGAGCAAA GTGCTATGTG GGTTT TAGAC 100

236

CATGACTGTT TGTTCGCTCT CCTGCCCTAC CACCAAGCAA AGCAGCAGGG 150
CTCCTGGGGG AGAGGGATTT CAACCCCCCT GATGGCAGGG GGTGCTCTGG 200
5 GGAGGAGAGA GGAGAGAACA GGCTGTTTTG GAAAATATCC AGCACTTTGA 250
C 251

(2) INFORMATION FOR SEQ ID :448:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :448:

20

ACACTCCAGA NCATCCCACT AGAAAAACAA TTNNCAGGA ACGTGATGGC 50
AACRAATCAGC AGCCAATATT CTCAAGAGTT CCTAATCACC AAAAACATAT 100
25 ACAATNTAGT CTAGAAAAAT AAGTCAATTT CATAAAATAA GTTTTTAGAT 150
CGAAAAGCAC CCCCTTCACA GGTACAGAGA TACTGAAAAA TAGTCCCTAA 200
AAATCTACTC ATAGTTTACG GAGAGAAAGG CATGCCATGT GAGTTACGGA 250
30 GTG 253

(2) INFORMATION FOR SEQ ID :449:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

237

(xi) SEQUENCE DESCRIPTION: SEQ ID :449:

ATATAAAAAA GATCCGCATA ATAAACCAAA TCAGAAAATA ATACCTTGTA 50
5 ATACCTCTGT AAGAAGCAGA ATACACCATA TGTATTAC ATGTATAGGA 100
GTGATAAGAA AAT 113

(2) INFORMATION FOR SEQ ID :450:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :450:

20

TAGCATCCAG GGGAAGTTAA TCAATACGCG AAAAATACTG AAATTAAAGA 50
GACAAGTAGA AGAAAATGAA ATAATCAAGA GATTGAGAAA AGTTGCCAGA 100
25 AAGCTTGGAG AAAAACCAAG ATATGTAATT TTCGCAGAAG TCAAAGGTAG 150
AAACTATTTG AGATCAAAGT CCTATAACA AAGTTAAATG ATTCCAAGAG 200
GTAAATAGGA G 211

30

(2) INFORMATION FOR SEQ ID :451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :451:

238

CTCCATTAGC TTTATGGGAC ATACGACGCA TAAAGATACT NTCCCGTGCG 50
NATTTACAC NTGNCAGAGC TATAAACCGG TGNATGATGT GATTTTNCCTG 100
5 TAGAATGATA TGGCCTGATA TGGAGGCCTC TTAATNGGCT TTTTCAAGCA 150
GCAAAATGGT CTTGNGTGAG TCGTGCCGAG GCTNNNGATC AAAG 194

(2) INFORMATION FOR SEQ ID :452:

10

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :452:

20

ACTTCAAGCT CAACCTATTC TCGTTCTCTT TGTTAGAGGT GTATTGAGGA 50
TAGCATATTG AGAATATATT CTCTGGTTCA AACCAAAGAT TTTGTGACAT 100
25 TAAAACTACT TGAATTTCTA CTCATAATA GGAGTCAGTC ACTTCTGGGA 150
CTATAGTGAT GCTTGCAA 168

(2) INFORMATION FOR SEQ ID :453:

30

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :453:

40

CGATTCTTGC CCTAGTCAGA GACTATAGCA GCCCCAGAC GTGAACCAAT 50

239

TGGCCATCTC CAGAAAGTTT AACAAAACCC GACCAGGTG CCCCCTTCAC 100
TTTCTTACAA CCTCTTCCCC TTCCCAGGG GCTCTGCTCC TCACTCCAGA 150
5 TCATCCTTTA GTTTAGAGCT GCGCAGTGAA GTGGATATCA CTGAAGGAGA 200
TAGGACGCCA GACTACACTG 220

(2) INFORMATION FOR SEQ ID :454:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :454:

20

GCCATCCTTG ATGGAAAAGA AACTGAAGAG AAAAGACAGC CTGTGGAAGA 50
AGCTCAAAGG TTCTTTGAAG AAGAAGAGAG AAAATATGAC ATGATATCTT 100
25 TGCTTTTGAG TTCCTCACGC TCTCTGAATN TTATTGGTTG GACATTCCAT 150
ATGTAGCATT CTGCTTCAAT ATTATCTATT ATGTGTCTCT CTCTCTTCAA 200
ATANNTGCCT GTAGGTAAAA GCAAGCTCTG CATATCTGTA CCTCTNGAGA 250
30 TAGTTTGGCT TTGTCTTTAG CGGTT 275

(2) INFORMATION FOR SEQ ID :455:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

240

(xi) SEQUENCE DESCRIPTION: SEQ ID :455:

TCGCAGAAGG AGGAACGGGG ACTTTCCATC CCCTGAACCA AGGCATGTTA 50
5 ACACTTGGCT CCAGCATGTT GTCATCATTC AACCAGAAAT CGCACAAATG 100
CTACTGTGCC GGGGTGNAGC CAATTTTCTT AAGTAAGTGC TGACTTCCTT 150
AACANNTATC TNTNTTNTGG CTGTAGGGTG GCTCAGTGGA ATCCATTTTG 200
10 TTAACACCGA CAATTAGTTG TTTCACACCC AGTGGTAAGC CAGAAGGGCA 250
TGCTCTNGGG TCTGCCCATT 270

15 (2) INFORMATION FOR SEQ ID :456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :456:

TCGCAGGAGA AGGAACCTTG ATGATACCAT TATCCTCACT TAGATGATGC 50
ACGACCCCTG CGCTGGATAC GGCGACGGTT TCTCATTTG CTTTGCCAG 100
30 CTCTCATTCG CTGAGGGGCA TAGACCTTTT GATATCATCC AGGCTTTAGT 150
TTCTTAAGGA GCAAAACAGC TTCCTTGNNC TTCTGTAGC CTTCAACTTA 200
35 TTTAACTAC CAAGGAAGTT CAGGAAGTTC CTCAANACGA TGACCTTTAG 250
ACAT 254

(2) INFORMATION FOR SEQ ID :457:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 base pairs

241

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :457:

ACACTAACTG TTCCATCCGT TATATTGCT GTGAGGAAAA TTAAGATTCC 50
10 TGTGTATGG GCTGCACTGT TTCTGGAAGA CTACAGAAAA TCTAACATGG 100
TTGACACTTC CTGGTAGCCC TTCTGTACAT ACACACACAC AACCAAGAGA 150
15 GAAGACAGAG AGAAAATCCT GGTCCAAAAG ATCACATGAC CTTACTAGTG 200
TTTCCCAAT GACTGTAATT TATAAACTAA AAATTG 236

(2) INFORMATION FOR SEQ ID :458:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :458:

30

GAGANNNTT NNGGNAAATG NTTNCGCACT GNAGCTAAGA ANAGNNATGG 50
NNNTAGGGNG NNAGANGNCN TGAACAGAGA AAGCNTGAGG GCTCTGGGAC 100
35 GCTGGTAT 108

(2) INFORMATION FOR SEQ ID :459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

40

242

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :459:

ACCCATGGCA AATAGGAAGA AGCTCAGTAT CGGCTCCTCC CACCATAACC 50
CCCACTTCTC CCGCCTCCTG GACCATAGTT TCCTCCACCA TACGGTCCCC 100
10 CCATGTTTCT GCTACCACCA AAGTTTCCAC TCTCCATTGG ACCGTAGTTA 150
GAGGT 155

15 (2) INFORMATION FOR SEQ ID :460:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :460:

TGCTATTTCC CTTTCATAAA GGCACACATT TGATCTTATC TTCTCTTACC 50
CAACACGCAG TGGCAGTGTG TATTTTCCTT CTCTTTTTTT GTTAAATATT 100
30 CTGGTTTGTG GAGGTTTACA GACATGTGTT AGTATATCCT TGCCTGCATG 150
TAGTTGTTCA TTACTAGAC 169

35 (2) INFORMATION FOR SEQ ID :461:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :461:

	ACCNTGTTTA ATTANTGCGC GGGCTCGCCG TTTGCATACA ATGGCTTACT	50
5	CAGTGCTNNC AGGCTGTGAG TNAATAGAGN GTGTATGACT TAATAAGCAT	100
	TTTATCAGCG TACCTTTTTC GCCATGCGCT ACCTGCTATT GATGAAGGCG	150
10	GCTTAGGGCA TCGAAAAACC TAAAAGTCGA GCTT	184

(2) INFORMATION FOR SEQ ID :462:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 275 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :462:

	AGGAACCNTG TTTAATTANT GCGCGGGCTC GCCGTTTGCA TACAATGGCT	50
25	TACTCAGTGC TNNCAGGCTG TGAGTNAATA GAGNGTGTAT GACTTAATAA	100
	GCATTTTATC AGCGTACCTT TTTCGCCATG CGCTACCTGC TATTGATGAA	150
30	GGCGGCTTAG GGCATCGAAA AACCTAAAAG TCGAGCTTNG NNGTGCCGGN	200
	AACGGCTCTA NANTACTTCT CATTGTAAGT AGAGTACCAT ATTCGGCCGT	250
	NNACTGNGTT GTTGGCGACA GATGT	275

35

(2) INFORMATION FOR SEQ ID :463:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 149 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

244

(xi) SEQUENCE DESCRIPTION: SEQ ID :463:

5 AATTCACTAT GCGTGGCCGC CACAGCTATN CTTGTCCTCC TGGATCCTGA 50
ACCTTGNAAG CTGCACTAAT GAGTTCAACG GGAGTGCTCT GGGCCCAGGT 100
GTCAGCTGTA GCAATGCCCC NGCTGCAACT GAAGNGCCA GCAATGCTA 149

10

(2) INFORMATION FOR SEQ ID :464:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :464:

ATCATCAGCA GTGTTGCTCA GCTCCTACCT CTGTGCCAGG GCAGCATTTT 50
25 CATATCCAAG ATCAATTCCC TCTCTCAGCA CAGCCTGGGA GGGGGTCATT 100
GTTCTCCTCG TCCATCAGAT CTCAGAGGCT CAGAGACTGC AAGCTGCTTG 150
CCCAAGTCAC ACAGCTAGTG AAGACCAGA 179

30

(2) INFORMATION FOR SEQ ID :465:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :465:

245

CTACCTCTGT GCCAGGGCAG CATTTCATA TCCAAGATCA ATTCCCTCTC 50
TCAGCACAGC CTGGGAGGGG GTCATTGTTC TCCTCGTCCA TCAGATCTCA 100
5 GAGGCTCAGA GACTGCAAGC TGCTTGCCCA AGTCACACAG CTAGTGAAGA 150
CCAGAG 156

(2) INFORMATION FOR SEQ ID :466:

10

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :466:

20

ACATCCCTGG AAGGAGGGCC TGAGGGCCAG GGAGGGAACA AGGCAGGAGA 50
CTGCTGGTTC TGGTTTTGGC CACCTACCC TTGGCCACGT CCCCTCCGGC 100
25 TAAGCCACAG CACAAAGCAG AGCCAGGCTC TGGAGGCCCA GGCCTCACC 150
ACTCCCCTNT GTCCCCCAG CAGGGGGACA AAACAG 186

(2) INFORMATION FOR SEQ ID :467:

30

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :467:

40

TNNNGATGAN TATANAAGCA TCATNGACGG TATTCCCG TCTTGNANTT 50

246

TNATCGAGAN TTTANTCTAG TAANTATATT AATNTNT

87

(2) INFORMATION FOR SEQ ID :468:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :468:

15 ACTAGAAGTA CAGCATCCTG CTGCAAAAAT GATTGTAATG GCTTCTCATA 50
TGCAAGAGCA AGAAGCCGAG ATGACACAAA CTTGCCTGG TATTGTGTTG 100
AGCTCTCCTG GAATCACTGA AGAACTTCTG AGGATCGGCC TGTCAGTTTT 150
20 AGAGGTCATA GAAGGTCATG AAATAGCCTG CAGAAAA 187

(2) INFORMATION FOR SEQ ID :469:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :469:

35 AGGGCACCAT TACCATCCAT CTGACATCGC ATTTCCATAG AAATGCCAAA 50
GAAAGAAGGT CCTGGGGTTT TTCATAGAAA GCTCAAAAAG TTCAACCTTT 100
GATGCTATCC CCCAGCCCAA TACAAAATAC ACAGAAAAAG CAATTATTAA 150
40 ACATCGGCTT CGTTTCTTTT TCNCCTTTGA ATNTTAATGT TTACATACTA 200

247

GTGTGCAGCA CCTACTTCTT NATCGCCGTG AACTGAAATC TAGATTTTAA 250
ACTGAA 256

5 (2) INFORMATION FOR SEQ ID :470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :470:

CTCAAAACGA CAATTCTGTG CCTGGGGGAT CTGACCTGGT GAGGTAGCCT 50
GAAGTCTGAA TGGAGCCCAT AGTCGAAAAC AACCTAAGAA TCTCTCAGAA 100
20 GAGGGTTTG 109

(2) INFORMATION FOR SEQ ID :471:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID :471:

35 GCGGCAGTAT ACAGAAGCCA TATCAGTTGG GAAAACTTT ATCAATCATA 50
GAGCCTTTTG AAGAAAAATT TGCCAAGCGT GGTTTTTGC TTGNAGACCT 100
ATATATATTA CCTACAGGCT GAGAAAGCTT TGNATTCT 139

40

(2) INFORMATION FOR SEQ ID :472:

248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :472:

10

TCGCAGGAGA AGGAATGTTT CCAATAGGAA CGCCTGTAGA CTGTTTCAGAA 50
GAAATGCCCA AATGAGCCAG ATGAGAAGGC TGAGGGCAGG GCTGCTTTTG 100
GCTCTGAGGA CTATAGATT ATCCTCTAGG TGATGAGGGA CTATTAACGG 150
CTGGTGAGTC TGGAGAACTG AACAGTGGAA GCTCTATTTT AGATTACCGT 200
GGCAGTAGAG GATAGAGGTG TTTGGAAGCG GTGGGCAGTT GCAAGCTATA 250
TGGGAGACAT TT 262

20

(2) INFORMATION FOR SEQ ID :473:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :473:

35

ACAGAAGGAC TTTGTCTCTT TAGCTTGTTT AGCTCAATGA ACATTATCTC 50
GGCAAATGAC TCTGCTTTCT CGAAGGTCCT TCTCCGCTCC AGGTTTACTT 100
GCATCTCTCA TACTTNNTAC AGCCAACATG AACACTCTAT GTATTTTCTA 150
AGCTTTCNTC TGTTCAAGAA CTTTGAATTT AAAACGTCT 189

40

249

(2) INFORMATION FOR SEQ ID :474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :474:

TNCGTGCCTA GCAAACCTAA ACTCGAACGC ACGTAATAGT GCTCATAATT 50
CTNTNAAGGA CTTTAAACTT TACTCNGTAT GCTNTNTTGA TGA CTCTAGC 100
AGCCTCGCTA ACCTAGTTTA CCCACTGTC CCCACCGGCG AACTNTTTGT 150
GTTAGTACGC GNGTTA 166

20

(2) INFORMATION FOR SEQ ID :475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :475:

TTTTTTTTTA GTAACACTAA AGAGCTGTAA AGAACATTGA AGGTGGTCAT 50
TCCTTCAAAA CTGTGTTTTG ACCACACAAG GTGGGCATTA ACAAACAAAT 100
TCAACTTAA 109

35

(2) INFORMATION FOR SEQ ID :476:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs

250

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :476:

TCTGGGCGGA AGGTGGTGCG GTGAAAGGTG CAGGGACAGA CTGGGTTAGA 50
GGCCACTCTT GGTCTTATCC TCCATGGCCA CAACAGAGGT GACAAATACA 100
CGGGTCACTC AGTTACGTTT AGCCACAGCC T 131

15

(2) INFORMATION FOR SEQ ID :477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :477:

ACATGGATAG GTGTATGCAT ACTACGGCTA AGGAGAAACA ATGTCCTAC 50
ATATATGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT 100
TAAAAATATG CAGAACTTAT TTCATCTGTG CTTTAGAAAT AACTGTATAC 150
AGTGTTATAA GTTGAAAAGA ACTCAAATA ACTAATACAA ATATACACTA 200
CGTATTAGAA TTCAAAAAG CTGCTTTCTG TGAAGTCAAT CAGCTATATT 250
AAAAAAGACA CAAAT 265

35

(2) INFORMATION FOR SEQ ID :478:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs

251

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :478:

AATCTACCAA CCTTAAAGCT CCCGNGATAA AGCTGTATTT CCAAAGACC 50
10 TGTNTTTATT NGNNGGNGTT NGCTTTCTTT GTCATCTAGA GCCTTGTTGT 100
ACATGCAATG GGTGGGAGAT AGTGGTACCT ACTGTTGNTT CTNTCTGTGT 150
15 NTTTCATCATG GTGTTGTCTA GGTCTCCTGA GG 182

(2) INFORMATION FOR SEQ ID :479:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :479:

AAGCCGTCGG GAGCCGCCGC CGCCATCTGA GGGAGGTACC CTGGAAACCA 50
30 CCTTTCACGG TGGGGAAGTG CAGTCGCGGT GGGCAGCTCT GGGGCCACGA 100
AACGGGAGCC TCTAAATCTT GGTCGGGACT GCTCGCCTGG AGCCGCACTC 150
35 TTGAGTCCGA GGCCATCTT 169

(2) INFORMATION FOR SEQ ID :480:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

252

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :480:

5 AGATAACGCT CCCATCCCAG GCTAGAGACT CCATCTCTAA TTTNCNCAGT 50
CCGTCAATGA GAGGCAGGGA CTGAAATCCC AAGTCTGTGTC TCACCGGATA 100
10 TTTTCCAGGA ATGCCTCTCT TCCAAACATC AGCGACATTT AACAGACCCT 150
GAGCAGCAAA CTTCTGCCCC AGAGGAAAGC AGAAAACCAA TTTATGTAAA 200
15 ATTAGAAGCG ATTTGCTTGA TCCATCACTN GCTTCCAC 238

(2) INFORMATION FOR SEQ ID :481:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :481:

TCGCAGGAGA AGAAATCAAC CCCTGCTTCT CAAATCCAGA CAGGCCACAC 50
30 TGGCTAGAAC TTCCACCCAG CAGTCCTGCT CCTGCCCGAA GTCTGCAAGC 100
AAGTGAACCA CATGTCGCTA TGAAAGCACA CAGACAACAG ATTAGGGCAG 150
35 ACCTGGCAAA GATATGCCTG TCTGCCATCT TGGCCCCTGT CTGAGGGAGG 200
C 201

(2) INFORMATION FOR SEQ ID :482:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

253

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :482:

	CGGCTCAGNC TGTTGGCGCG AAGAGAGTCT AACCCAAAAT TGCAAAACTC	50
10	CCGTTGATTT CCAGGCCCTA CCACACGGCG ATGTCAACTT GTCCTCCAGA	100
	CATGGACGAC TACCAAAGAT CCCAGCTACG AAGCATGGCC TTGCTTAGAA	150
15	ACNTTTTATG AT	162

(2) INFORMATION FOR SEQ ID :483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :483:

	ATATGAAGGA GGAAATGCTC GTCACCTTCG TGAATACCAA GACCTGCTCA	50
30	ATGTTAAGAT GACCCTTGAC ATGAGATTGC CACCTACAGA AGCTGCTGGA	100
	AGGCGAGGAG AGCAGGATTT CTCTGCCTCT TCAAACNT NCCTGAACCT	150
35	GAGGGAAACT TTGGATTCTC CCTCTGGTCG ATACCCACTC AAAAAGGACA	200
	CTTTTGATTA GGACGGTTGA AACTAGAGAT GAACGGTTAT CAACGAAACT	250

(2) INFORMATION FOR SEQ ID :484:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs

254

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :484:

AACATTATCT TGACAACTG AAGAACACTT CAGTTAACAC TACCTCGAAG 50
AACCATCAAT GACTTGCTTT GAACAGACTA TAAAGGCAT TCTCAAGGAG 100
ATTAGAATGT TAATGCCACT TTGATTAGAT CT 132

15

(2) INFORMATION FOR SEQ ID :485:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :485:

TGTGCGTGGA GACGGTGGAG AGTGGAGCCA TGACCAAGGA CCTGGCGGGC 50
CGCATTACAG GCCTCAGCAA TGTGAAGCTG AACGAGCACT TCTTGAACCC 100
ACGGACTTCT CGACACCATC AAGAGCGAC 129

30

(2) INFORMATION FOR SEQ ID :486:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

255

(xi) SEQUENCE DESCRIPTION: SEQ ID :486:

TCGCAAGAGG AGACATTCTG ATCATCTCA CTGGACGCCA CAGGGGCAAG 50
5 AGGGTGGTTT TCCTGAAGCA GCTGGCTAGT GGCTTATTAC TTGTGACTGG 100
ACCTCTGGTC TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT 150
CATTGCACTT CAACCATATC GA 172

10

(2) INFORMATION FOR SEQ ID :487:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20.

(xi) SEQUENCE DESCRIPTION: SEQ ID :487:

ATGCTGCACA CTATGTCTCA CAACTAAAT GGATCCATTA AAAGTTATGA 50
25 TTTAAAAGGC GACCACCCCC AAAAGAAGTC ATAACACTCA AGGGTGTCAA 100
TATATACAAC TGTGTAAACA CAACCAATCT ACAACTATAT CAACACAACC 150
AGCACTCCTC TATGGGCACA GACACACACA CAAAATTGTC CTTGCTTTTC 200
30 TCAGATATAT 210

(2) INFORMATION FOR SEQ ID :488:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

256

(xi) SEQUENCE DESCRIPTION: SEQ ID :488:

ACATGGATAG GCGTATGCAT ACTACACTAA GGAGAAACAA TGGTCTACAC 50

5 ANACCTAGTG AGAACATTAT CTGTATACGG GAACTGTGAT 90

(2) INFORMATION FOR SEQ ID :489:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :489:

ACCATGAGAC CTACATCCGA ATCTGACCCA GGCAAACATA CCGGGAGCCA 50

20 TACCGCACTA NCGGCTCTTC TCAAATCTCC TGGCCACNCA CCGAGNGCC 99

(2) INFORMATION FOR SEQ ID :490:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :490:

35 GGAAACCTGG AGGTGCGCAT CCTCGAGTGC GAAGAGAAGG TCTTCCCCAG 50

CCCCCTCTGG ACTCCATGCA CCAAGGTCAT GGCCAGGAGC TCTTGGCAGC 100

TCAGCCCTGC CGCCCCAGAG CATGTGGCGG CTGCTCTCTA CCAGCCGAGA 150

40 GCTTCGGAGA TGCAGCATCT GCGGCGAATG CCCCCG 186

257

(2) INFORMATION FOR SEQ ID :491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :491:

AGCCAACTAA GTTCTCTCTT CGTGAAACAC AGGTCCATGA GTCGACACAA 50
ACACTAATGC AAGAACCATC ACGGAAAACC ACCGCAGCAG CTGAAACTTT 100
TATAGCCCAT AAAAGGACCA AACAAGTAAG CTGAATGACT GTGAAAATAT 150
GACCTTCCAG AGCGGCACAT AACAGGATAT CAAATCAGGC TGATGCTTAG 200
CAGGCTTCAA ATATNATGGT CAAATGACTG GATTACTTAN ATGAGGCAAC 250
TTCATATCGG AAA 263

(2) INFORMATION FOR SEQ ID :492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :492:

AGAGTGGGGT TAGCTCTGCC TAGCGCTACA CAAGAAAACC TCCCTCCAGT 50
AAATNGGTGT GGGNGGTCCG CTTTTGGCCA TCATCGCACC CCCCCGGTCA 100
CTGGGCGTTG TTGCCGGGCA CTTGTTTNNC NGGCTGGGTG TGTACCGTAA 150

258

159

CCGTGGGTC

(2) INFORMATION FOR SEQ ID :493:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :493:

15 GGGCAGAGNA AGAACTGTTC CACCAGGTGA ACAGTCCTAC CTGCTTGTA 50
CCATAGTCCC TCAATAAGAT TCAGAGGAAG AAGCTTATGA AACTGAAAAT 100
CAAATCAAGG TATCGGGAAG AATAATTTCC CCTCGATTCC ACAGGAGGGA 150
20 AGACCACACA ATATGTNGTG CTGGGGCTCC CCAAGGCCCT GCCACCT 197

(2) INFORMATION FOR SEQ ID :494:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :494:

35 GATGGGGAAG GGCATCCCAA CACAGCCTGT GGATCCTGGG GCATCTGGAA 50
GGGCGCACCA TCAGCAGCCT CACCAGCTGT GAGCCTGCTA TCGGGCCTGC 100
CCCTCCAATA AAAGTGTGAG AACTCCACTG TGTGCCCTGT CTTTGGGCAG 150
40 GGAGGGCTGC TGTGAGTGGA GTCTTGAGTN GGTGAGTG 188

259

(2) INFORMATION FOR SEQ ID :495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :495:

ACATGACCAT CCGCATCCGC CTTTATTGAC AATGAGAAGA TGGAGTCCCG 50
GACGCATCTA TCCCTCTTTG GCCCTTACAG GTTGCCACG AGAGTGAGAC 100
GCCTTCCTGG ACCAGGGGAG GGNNGTTGG TNCTNTGNGC GTGNGGGTNT 150
GTGGGNGCTG CTGGGGAGG 169

20

(2) INFORMATION FOR SEQ ID :496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :496:

CAGAGAGAAC GTTCTATGG CTGCTGCTC TAGGAGTCTC TCGCTCATAG 50
AAAAGGCACA CACTGAAAGA GGAAGCAGAT CCCATTGCTG TGGAAGTCCC 100
ATTGTTAGGA AGCTCTGCTT TTCTGGAGTT CAAATTCGCA TTCATGATGC 150
TTTAAACCGT CAAGCTGGGT GG 172

40

(2) INFORMATION FOR SEQ ID :497:

260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :497:

10

GAGAGTGGGG TTAGCTCTGC CTAGCGCTAC ACAAGAAAAC CTCCCTCCAG 50

TAAATNGGTG TGGGNGGTCC GCTTTTGGCC ATCATCGCAC CCCCCCGTC 100

15

ACTGGGCGTT GTTGCCGGGC ACTTGTTTNN CNGGCTGGGT GTGTACCGTA 150

ACCGTGGGTC CTCTGACAAG TGCCTAACTC GGCCCACCCC TTAGGGTGTG 200

TNTCATCGAA GTGTAGNGAA TGGTGGAACG TTTGTTTGTN GTGTGC 246

20

(2) INFORMATION FOR SEQ ID :498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :498:

GCCCCCTTAC CAGCAAGTCC TCTACTCAGA AAGAACTGAC CCACGCAAGT 50

35

CTGGGAGAGT GACTAGTTCA AATGTGCAGG GCTGAAGCTT CCAAACACAG 100

CCACTATTTT TGTTGTATAT CTTCATCTCA ATGGCGACAT GGCCACTGCC 150

CAAGGAACTT GTGGCAGGGA TCCCAAGGTG AGGCAGCAAC AGATGTCTGT 200

40

GAACATCGTG CGTTA 215

261

(2) INFORMATION FOR SEQ ID :499:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :499:

GATNGCCACA TCTCAACACT ATACNACTCG CTNTTCGAAT TCGCCGTNTT 50
15 AGAACCGCAA GAGACCTTGA TTTAGTCACG CGAGTTCGTC TTCCTGTTCC 100
ACANGAAAT AAAGCTAGGG AGGTGATTTA TCTATCCGAG AAAAAAGCCG 150
GGGACTGGTG GAANNNGAAC AATGNTCTCT NTGTCGTACT ACAAT 195

20

(2) INFORMATION FOR SEQ ID :500:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :500:

GCGGCCTTGG GGGCACCGGC GTGTCCTGCC CAGTGGGATT AAAAAATAAT 50
35 GCTCCCCACA TGGCGGGCCT TTGAGGTTCC AGTAAAAATG CTTTCAACAA 100
ATGGGCAATG CTTGTGTGAT TCACAATCGT GGCATTTAAA GTGCACAAAG 150
TACAAAGGAA TTTATACAGA TTGGTTTACC GAAGTATAAT CTATAGGAGG 200
40 CGCGATGGCA AGTTGATAAA ATGTGACTTA TCTCCTAATA AGTATGGGGG 250

262

260

GTGGAGCTGT

(2) INFORMATION FOR SEQ ID :501:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :501:

15 AAAGGCATAG TAAAAATAAA ATCTACGTAA GTAACAATCT AATACTATAT 50
TAAATNCGTT GCTACAAAGT GTTTTGTTC TCTAAAAAGT AGTTTTTGCA 100
TATCATTGCA CCTCTTCACC CATNTGCTGG CTTATTGCT TTATATACAA 150
20 CAGTTAAAAT TTGTGCACTA AGCTGAGCTG CCTTCACAAT GTGGTTCAGA 200
CAAAATGCAC CCAAAGAACT ACATGTTAAG AGAGTTTATG TCCATGCTCA 250
25 ACCATGGCTT GCCCAAAT 268

(2) INFORMATION FOR SEQ ID :502:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :502:

AAAACTCTA ATCCAGACTA CAGTTGTCGA GATTCAAGTC GTGAGTGCAG 50
40 GAGCGTACAC AGTGCCGTGC TGGCACATGC ACTGCACACG CTCTAGAGAC 100

263

GCTGACCTGG CTCTCGGAAA CGCAGGAGTC TTTCTGAGCC AGCTCAGAAA 150

CC 152

5 (2) INFORMATION FOR SEQ ID :503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :503:

CCCTGACCCC TCCTCACCAC CGCGCTGCAC CTCAGGGTTA CAAGAAGAAC 50

TAGGAAATAA CGCCGGCCAC CNGACCCCTG GAGAGGGGCC GGCTAGAACA 100

20 NTTCTAAGAT CCNGCACAGC AGGTCCCGNA TGTNGAACCT T 141

(2) INFORMATION FOR SEQ ID :504:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :504:

35 CACACGACAC ACGACACGCA CGCAAACACG CCAGACGCGA CAGAGCGCGC 50

GCGGGAGCGG AGCAGCGGAA GCGCAGCAGC GCACACGAGA GATAAGGGCG 100

GCCGAGC 107

40

(2) INFORMATION FOR SEQ ID :505:

264

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :505:

10

ACCCTCTTCT GATAAATTG AGGGCCCGTT TGCCTTGA GACCTTCAGT 50
AACTCCATGG CGCGCCATCG TACGGGGCAA ANACACACCT CCCGAATCAT 100
GTCCCGCACG AACTGGTGT GTTTGGTCAG ACGCCCGCGT TNGGCNTGTG 150
CTGGGCTTGC TCACGTTCTT GTCACCTTGT GGCCCTTGTT GAG 193

15

(2) INFORMATION FOR SEQ ID :506:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :506:

30

ACATGGATAG GCGTATGCAT ACTACGCTAA GGAGAAACAA TGTCCTACA 50
TATTACGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT 100
TAAAAATAGC AGAACTTATT ANCTGTGCTT TAGAAATAAC TGTATACAGT 150
GTTATAAGTT GAAAAGAACT CAAAATAACT AATAAATATA ACCTATGTAT 200
TAGAATTAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA 250
TGACACAAAT CCAAACAAGA TGCA 274

40

265

(2) INFORMATION FOR SEQ ID :507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :507:

CAGGAGAAGG AAGGTTGTAC GTGGACACTA TAAAGGTCAG CAAATTGCAA 50
AGTAGTCCAG GTTTACAGGA AGAAATATGT TATCTACATC GAACGGGGCA 100
GCGGGAAAAG GCTAATGGCA CAACTGTCCA CGTAGGCATT CACCCCAGCA 150
AGTGGTTATC ACTAGGCTAA AACTGACAAA GACCGCAAAA AAACCTTCAA 200
CNGAAAGCCA AATGTNCCAG CCGGAAAGGA AAGNGCATAC AAGGAAGAAA 250
CCATTGAGAA GATGCAGGAG TAAAGTATTA T 281

20

25

(2) INFORMATION FOR SEQ ID :508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :508:

AGGGNTGCTA ANNTATTGGT GGGCAGGAGG CATCGCTGAT GATCTTGAGG 50
CTGTTGTCAT ACTTCTCATG GTTCACACCC ATGACGAACA TGAGGCATCA 100
GCAGAGGGGA CAGAGATGAT GACCCTTTCG CTCCCCCTG CAAATGAGCC 150

40

266

180

CCAGCCTTCT CCATGGTGGT GAAGACGCCA

(2) INFORMATION FOR SEQ ID :509:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :509:

AAATGCAAAA CTCACCGTGC AACTCCTAG ATCCCTGCCA CAAAGAAATC 50
TTTGAAAAAT GAAGTCTTCC TTTCGGACAA TATACCATTN GAGTTTCTCT 100
ATTT 104

(2) INFORMATION FOR SEQ ID :510:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 171 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :510:

GTNNATACAC AACTAAGTTC AAATAAAAAA ACCAAATNAA AAATNGGCAG 50
GGAAGCTAGA GCCAGAATCA GGAAATCTG TTTCCTCGTC CCCAGACTCC 100
CGCCAAGCCT ACTCCACTAA CTAACANNGA CTCTATCAAG TTTCTATCAA 150
GACTTGCATC TGNATCTTGN A 171

(2) INFORMATION FOR SEQ ID :511:

267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :511:

10	ACTGTACCTA TCATCCTGAA AAACCTTTATG GGGGAGAAAG GTCAGCAGCT	50
	TCTCTTTCTT TTNATCGAAA ATAATAAAAC TGCCTATTCT ACTTTAACTA	100
15	AATGTAAGGA AGAAAATATA CAAGCCCATATA TTTAATGTAT TTCTATNCGA	150
	GCAACAATAG TTCATATGTT CATGTTTGCT ACTATCACAA TTCAACATAT	200
	GAACACAGAT CAGCTCTATA CCATGAATAC TGCTGGAAGT GATGGTTTAG	250
20	GATTA	255

(2) INFORMATION FOR SEQ ID :512:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :512:

35	GAAAGATTGG ACATGATTGC GTTTATAAGA ATGAGAGTGT TAAATTGGAT	50
	TTCTTGCTTT ATTTGTGACA TTTCAGTTTA TTAGAAATCA TGTTACCATT	100
	AGAAAAATTG AAGTTTCCTA GTAACAAAGT AATTGATTT GTGTAAGTTG	150
40	ATAAAGATT TACTGACTTA AGCTTTTGTT TTTTTCATA AGCTGCTTTT	200

268

210

GAGCTTTGTC

(2) INFORMATION FOR SEQ ID :513:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :513:

15 CTGTACAATC ATCCTGCAGA AAATTGTTTT GGAGAATTCT TGGTAATTGA 50
AGACCAGCAG AGCACCCCTC CCCACCCGCC CCGTAAAAGT GCTTACAATG 100
AACAGGGATT CTTTCTTTA CAAAAGACCC AAAGATACGT GGACAAAAAA 150
20 AGAAAAGCTT GAAGTCTCAA TGCCTAATGT GTGCACATAA AACAGGCACG 200
AAGAAACAAA CGTGTGCATC CT 222

25 (2) INFORMATION FOR SEQ ID :514:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :514:

GCAGGAGAAG GAAAAGACAG CAACTCATCC CAGAATTGCC NAATGAAGAT 50
GAGGAGAATC CCCTCAAAGG GATCTGTGTG CTTACAGTGG TGACAGTGAC 100
40 AATGAGGAGG ACTGATGAGA GACTCAAGAG TGAGGAAGAG AGCTAGCTGA 150

269

CTGNAAGAAA TGACCTGTCT NNTCTNCAGC GCCATTCCCN AACAGATGCC 200

CTAGTCAGGA CCACAACCTCT TAAACCTCAT AGCNAAATAT 240

5 (2) INFORMATION FOR SEQ ID :515:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :515:

CAATGCCCAA TCTGAGTGTA TACACATCTT AGGAAAAATA ATCTAANGTA 50

ACTTTTGAGG GTGAGAGNGG AAATAAGAGA TCACATTAT TCAAGACTGA 100

20 TCCCTATNAG GAAGGAGAGG CCCAGGCACA GATACCACAA AAGAGCACAG 150

TACCCAGCTG TCCTGGNATT GNTTGAGTGT AAG 183

25 (2) INFORMATION FOR SEQ ID :516:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :516:

TCGCAGCAGA AGGAAGTCGT TGACCTGGCA GCCAAGGGAA CACACAAACA 50

CACTCACACA CACATGCACT CACCTGCATA CACACACACT CATAACACCG 100

40 AACACTCATA CACACANGCT TGTGCACACA TGTTTCATGCA CATGCATGCA 150

270

CTCACACTCA TACAAACGCA CATTAAACA CGTGTGNACA NTGTACTCAG 200
ACACACACAG GTGTG 215

5 (2) INFORMATION FOR SEQ ID :517:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :517:

TCGCAGAGAA GGAACAATCA GGGCCATGAC AGGAACCGCA AAGAACCAGA 50
GGGTATAGGC AGCAAAGAAG GGCACATAAA AAGGCTGCTT CTCAGGAAAG 100
TGTCGCAGTG AGACAAACAC ACATACAGAC CACACACAGA CCACCACCTC 150
AATCATGGGC CCTAGCCGNC CTNGTAATAC G 181

25 (2) INFORMATION FOR SEQ ID :518:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :518:

ATGTAACTCA ATCCATCCGC AAGAAAACCA AACCAACAGA AAAGGAAGCT 50
GAAGACATGG ACATCGCAAG CCACGCGGTA ATGCATACTT GGCACAGAGT 100
AGCCAATATA GAAGACGTGT GCCTCACACG GTTCACTTTG TTCATCAATA 150

40

271

AAAGAATATA AAAATCTCGT TCACCCAGTG GTAAGTGTAT TAAAATAGAT 200
CTGTATCATA CACACAGTTT CTCCCGGAGT CGTGAGAATG ACAGGAGGGA 250
CCTGGCAACT 260

(2) INFORMATION FOR SEQ ID :519:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :519:

AAGCTAATAC AATGGTCATT TCCAGACAAA TTAAAGGAA AACTAAGGC 50
20 TGCTTCAAAG ATTATCTGAT TCCTTTAAAA TATATGTCTA TATACACAGA 100
CATGCTCTTT TTTA 115

25 (2) INFORMATION FOR SEQ ID :520:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :520:

CANGTGGCTT CAATTAAACA ATNAGGAGCC TCNNAACATC CTGTCGCAGA 50
AACTCCCAAT ATAAACGCCC CCANACACTA ACACAAAACA GCCTTATTAA 100
40 CCAGATAAGT TCTCCACTAC CACTCCTAGA TTTGATGTAA CCCTGAATNT 150

272

175

GACTNATAGN TNGACCCACC TGTGA

(2) INFORMATION FOR SEQ ID :521:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :521:

15 ATGGAATCAA ACAGCTCTAT AATGAAGATA ATGTCTCAGA AAATGTGGGT 50
TCTGTGTGTG GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG 100
TCCACCTTTG CAGCCTGTTT CTGTCATGTA GTTTCA 136

20

(2) INFORMATION FOR SEQ ID :522:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :522:

35 AATGGAGCAA TTCATCCAGT TCTTCTAGAA ACAGCTCAGA ATCAAAGCTG 50
GATATATTTT GTGTCTTCTG TGACTGTTCA TTCATGGAAG GAAGCAGACT 100
GCTTTGGGCA GAATTATTCT CCTGACTACT TGAGCTAGTA GACTAGGAAC 150
TATTCCATAA GAGGAAATCC TGTAAGTCTT AAATCCCCAC TGGAGAAAGC 200

40

(2) INFORMATION FOR SEQ ID :523:

273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :523:

10

AGTAAGGTTT TGCATCCTTT GATCAGCAGG TAACTGACGA ATTCTTGAGT 50
CGAAGATTAT ACCTTGATGA GCTTTGATGA GCTCTTGCAA ACGAATGAGA 100
CCAGTGCTGT CATCATACAC AACCATGACG TTTTCCACTT GAAAACTGC 150
ACCAGGTCTA AAATGCACGC TGAGTGAAGA GAAGTCTGGG CAGAGACTGA 200
CATA 204

20

(2) INFORMATION FOR SEQ ID :524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :524:

ATATCTGTCT CATCATCCCA AGGTTTCACA TCTAGTAAGA TGGAAGACTT 50
GGCAACAAGT GCAGGTTTTT TGGCTTTCTT TGATTCATAT TGTGCAAGAC 100
GTTCTTCCCT CAGCCTCTTT GCTTCTTCAC TTNNTCTAAN ATAATCCAAA 150
GAGGTCAATG TATCATCA 168

40

(2) INFORMATION FOR SEQ ID :525:

274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :525:

10 AAACTGTTCT TTAAAAGGCC TCTCCTGGTT ATTAAGCCAG GAAGAGAAGT 50
 AGAATCTCGA ATCACCTAAN GGAAATGGTG ACACAGGTTG TCCTTTCTCA 100
15 GCCGTTGGTT TCCTTTCATC TCTGAAGGCC TGTAGTACCA TGAGGAAAAC 150
 ATTTAATTTA GAGGGTGAAC CCAACAGTAG GAAGCTGAAA GCAGAAGTGT 200
 TTATCTCCCT CTGCATTGAG ACCAGGCTCC TTAGTGCACT CATCAGACTA 250
20 TCGCTGCCCC TGCTGTCTGC TGTTGAGCCT TCACCACCAC T 291

(2) INFORMATION FOR SEQ ID :526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :526:

35 CATCCGCGTG CTGGACCCCT TCACCATCAA GCCCCTGGAC AGAAAACCTCA 50
 TTCTCGACAG CGCTCGTGCC ACCAAGGGCA GGATCCTCAC CGTGGAGGAC 100
 CATTATTATG AAGATGGCAT TGGTGAGGCT GTGTCCNNNN GTAGTGGGCG 150
40 AGCCTGGCAT CACTGTCACC CACCTGGCAG TTAACCGGGT ACCAAGAAGT 200

275

GGGAAGC

207

(2) INFORMATION FOR SEQ ID :527:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :527:

15 AGCATTCCGT AAGGACGGAC GTGTTCAAGG ACAACTTTGA TGAGATGGAC 50
AGGTCTAGGG AGGTTGTTCA GGAGCTCATT GATGAGTACC ATGCGGCCAC 100
CCAGCCAGAC TACATTTCTT GGGGCACCCA GGAGCAGTGA TTTCCCTCCC 150
20 CACTACTTCT TTNCTTAGAT GGTAACCACA GCCTCGACCA TGCCTGCTCC 200
CTCTGACCCA GCTTCACC 218

25 (2) INFORMATION FOR SEQ ID :528:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :528:

AACCTNATGA CTCTCCATCC CTTGAACCA AACATCTAGC ACTCAGCTCC 50
AGCATATTTT ACCATTCAAC CCGAAATTCA CAAACGCTAC TTGTCGACTT 100
40 GTAACCAATT TACTCAGCAA GTGCTGACTC CTTAACGGAT CATCCCCATC 150

276

CTNCGCTGCA AGGTGACTCA CTAAAATCAT NTGTTAACAC CAACATTATT 200

TTTACACCCA GTGTGTAAGC CAGAAGGGC 229

5 (2) INFORMATION FOR SEQ ID :529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :529:

ATATTATTCA TCATCCCAAG GTCACATCTA GTAAGATGGA AGACTTGGCA 50

ACAAGTGCAG GTTTTGTCTT TCTTTGATTC ATATCGTGCA AGACTTCTTC 100

20 CTTAGCCTCT TTGCTTC 117

(2) INFORMATION FOR SEQ ID :530:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :530:

35 TCGCAGCAGA AGGAAGCTGA TCCACCATCC GGACAACCCG AACCCAAGCT 50

GAAGACGAGA AATGATCCAG AAAGAATGTG CTGCAATCCG GTCATCTTTT 100

AGAGAAGAAG ACAATACACA CCAATGTCGA AATGTGGCAA AATTACTGTA 150

40 TATGCACATG CTGGTGCTAC CCTCTCACT 179

277

(2) INFORMATION FOR SEQ ID :531:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :531:

AAAGCATTCA AGTAAGAATA TGGCAATAAA AAACAAAAT ATCTTCTCAG 50
15 CATTCAAAAC AAAACGCATA AGTCATTCCT AACTTNAGAG CTTTATAGCA 100
TTTTCCTAGA CAGGAAGGGA AAAACAGTT AGCATTTAA AGTCCGGAAA 150
GCTTTTTCGT TGNNTTAATT ACATCAACNN TCTGCCTTG TCCAAATCCC 200
20 TTAT 204

(2) INFORMATION FOR SEQ ID :532:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :532:

35 AAAGGAGCTC AGAAGTTCAG CTTGAGCAGG AAGAGGAGGA CGTGCCAGAC 50
CAGGAACAGA GCAGCAGCAT CGAGACCCCA TCAGAGGAGG CGGCCTCTCC 100
CCACAGCTGA GGGGCTGGGC TAGGGGTGGG TGGAGCCCTT TTAAATACC 150
40 CTTTCTCAA AACTTAGCTC TGAATGGAGA AAC 183

278

(2) INFORMATION FOR SEQ ID :533:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :533:

GAAACAAGTT CTCGCTCATC CCTGCATTTT TGCCAACTTC AGCTTGCAAT 50
15 ATTTATACTC CAGACTATTT TCATCAGACA AAAACCAGTA AGCAGGGTCC 100
TCTTTGAGAA GAGTTCTCTC TTTGGGAGAC AGGCTGCCTT CGATGACACG 150
TTTCACAAGC TGGTTGATGG TGCCCACTAC CCGTGATCTG CTCGCTGGGG 200
20 GACAGCATCA CTCAGACTAC TTGGAGCCTT GCCTGAATTT CAGGTTTCGT 250
AGGAGGAATA ATTTTCTCCT TCTNTNGTAT CGNCTCT 287

25

(2) INFORMATION FOR SEQ ID :534:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :534:

AGCCACTGCC CCTCTTGTCT ACGTATTCCC AAAATTAAAC TTTGATGCCT 50
GACTTTTTGC AGTCAGTTTT AAGTGAGCTC CCTGAGGTGC CAAGGCCATG 100
40 GTGTCCCCCT GCTGCGTCTG TTCGTCAGCT GAGTTCTTGT GAATCTNTGT 150

279

TTAG

154

(2) INFORMATION FOR SEQ ID :535:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :535:

15 GATTACCCTA TATCTACAAT TNGAGGTAAA ATAGAAGCAA CACATAAAAG 50
GGCCTATTTC TGCTACCATG TCATATAATT CTCCATAGTG AATATTGTGA 100
TAAAGCTACT GAAAACTATG CCTCACAGAG CCTAGCTTCT TGTAGAGCTG 150
20 GTATTTTACA ACTCGCATTG CTTGGAAATC TCAACACACG TAAGACTCTC 200
CTAGGAAGGC AC 212

25 (2) INFORMATION FOR SEQ ID :536:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :536:

GGAAGCTCAA TGTCGGCAG GTCAATGCTT CNCGGACACG GATCATTTTT 50
ATCTGATTCC AGCCTGCTTG CAACCCTGGA ATCCTCTTGT TCCCTGCTGC 100
40 CTGCCCCTTG GGAAGGNA CA GTGATGTCTT TAGGGGAAGG AGGAGCCCCCT 150

280

168

NTCGGCAGTT GTCTTACT

(2) INFORMATION FOR SEQ ID :537:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :537:

15 CGGATCATTT TTATCTGATT CCAGCCTGCT TGCAACCCTG GAATCCTCTT 50
GTTCCCTGCT GCCTGCCCT TGGGAAGGNA CAGTGATGTC TTTAGGGGAA 100
GGAGGAGCCC CTNTCGGCAG TTGTCTTACT AGGNNNTAA TGAAGTA 147

20

(2) INFORMATION FOR SEQ ID :538:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :538:

GTGGAATCTC AATAATGACA CAAGGTACCA ACTGCCAGCA TTTCTGCGAG 50
35 GCAATCCTGC TCTTAATCTG CAAGATGGAC CCTTCTGCAG AGAGATTGCT 100
GTGGGTGATT CTAAGGACAG ATTGTTATAT ACGATGTGGG AGAGCAGATT 150
GCTGTTCCCC GCAATGATGA ATGGGCACGG TTTGGCCGAA CACTTGCAGA 200
40 AATNAATGTA AACCNAACT GATGTAGAGA GGACGCAGCT GCCCNAATAC 250

281

(2) INFORMATION FOR SEQ ID :539:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :539:

AGAAGGTAAG GGAGTGGGAG GCAGGTGGGT GTTCTGGAGG GGGTATCCTT 50
15 GTGCTCTAAG GGTGCTATGT TCGATGCTGG TGTTTCGGGG ATGGTGAATG 100
CCCTTCTTTA ANNTTAGAGG GAAATCCAAA CCAATAGGCC CCAAGGTTGC 150
CAGTGGGATA GGGGTGTAAA AAAGTAAATT GGGC 184

20

(2) INFORMATION FOR SEQ ID :540:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :540:

AACTTATAGA AAAGTAAAGG AAACCCCAAC ATGCATGCAC TGCCTTGTGA 50
35 CCAGGGAAGT CACCCACCGG CTATGGGAAA TTAGCCCGAG GCTTANCTTT 100
CATCATCATG TCTCCAGGG NGTGCTTGCA AAGAGATATT CCGCCAAGCC 150
AGAT 154

40

(2) INFORMATION FOR SEQ ID :541:

282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :541:

10

AATTGAATTC TTAAGAAGCT GTCAAATATG GCAGTCTTTT GATGTTAGTA 50

ATTTTGTTTT CTTCTGTGTT ATTGGTTCAA AGTACTGGCC TTTTCCTTCA 100

15

TTTCCAGTAA TTATTTTATA ACTATCACTT TTAATTGAGT GGAAATTAGA 150

TGATTGCTT ATACTGTGAA ACAGC 175

(2) INFORMATION FOR SEQ ID :542:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :542:

30

AAGTACCTTT TCCTGCAGCT GCCCGTATGC CTGAGTGACT AAGGGGCAGT 50

CGTGAGAGGC AGAGTCCAAG ATCTCATTGG TCGTTTCCAG ACTGCCGTCC 100

35

AGCCGTGCTG CTTTCATCAGG GCACACTCGC CGCCCTCCTG GGGCCAGGTT 150

GCACATGTAC AGGTACCCGT CGGCGCACCC ACCAACAACG CGGTCTTCTG 200

AATCGCGACT GGCNAACAGA T 221

40

(2) INFORMATION FOR SEQ ID :543:

283

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :543:

10

AAGTAGATAG CTTGCATCCT GACACCGTGG CAAAGTTAAG AAAGTTGAAG 50

GAGAAACATA CCTTGAGAGG GGGTTTCTT TAAACTAGT GTTAGAAGCT 100

15

TAGGGATTTT TTTTTTTATT CCTTACTAAC TTTCACCCAG AACCGCTCTA 150

TTTGACTTGT GCCGACATTG CAACTTTNT GACAGG 186

(2) INFORMATION FOR SEQ ID :544:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :544:

30

AGCATCCTTG CCACCTCCCC ACCCGGGAGT CAAGGGTCGT GGTCTGCCT 50

TGAACAGGCC ACAGCCGTAG CTGTAGAGAG GCCAGTGGTA CATCAGCCCA 100

35

CCGACAGGAG GAGGAGCCCT GGCTTGAGGG AAGGGGAAGC CCAGGCCTGT 150

GCC 153

(2) INFORMATION FOR SEQ ID :545:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 base pairs

284

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :545:

	GATTCAGCTC CAGCATCCTT GCCACCTCCC CACCCGGGAG TCAAGGGTCG	50
10	TGGTTCTGCC TTGAACAGGC CACAGCCGTA GCTGTAGAGA GGCCAGTGGT	100
	ACATCAGCCC ACCGACAGGA GGAGGAGCCC TGGCTTGAGG GAAGGGGAAG	150
15	CCCAGGCCTG T	161

(2) INFORMATION FOR SEQ ID :546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :546:

	AATAGCCCTG AGGTCATCCT GCAAAGTGCG TATCAAAAAA TACGAAGTTA	50
30	GGGTGACAAA GTTTGACAGT GATGTTATAC AAGTCAAAC TGAAGGTCA	100
	TAGTAAGCAT ACCTATGCTG AGAGAAAGCA TCAAATCCTT TGTGTACACA	150
35	TTTAGTTTTA TTGTAACAAA GCAACTTGTA CACTTTTA	188

(2) INFORMATION FOR SEQ ID :547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

285

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :547:

ATNCCTTCTC CATCCANTTA GTTANCAGAA ACTAATCAAA AGAAAGTCTG 50
ACAACTGCAC TCCCCCTTGC ATGCCATTCT CTCAAGCCCA TAATCTTGGA 100
10 GTATCCACAA CGTGCGAAGG CCTACCCTTT GTGTGTACTC ATCTCACGTT 150
TACGTATTTT GTNGTTGAGG AGCTCCTCTA CAAATGTTGC GTATCTTCCG 200
15 AATCACTCAT TTAGAAAA 218

(2) INFORMATION FOR SEQ ID :548:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :548:

GGAGGAGACC ATCAGNCCCG TGAAGACCAC TCCTGACGTC TCGTGT 46
30

(2) INFORMATION FOR SEQ ID :549:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :549:

286

AGGGGGCTAA NGGTTGGGGG CAGGAGGCAT TGCTGATGAT CTTGAGGCTG 50
TTGTCATACT TTTCACGGTT CACACCCACG ACGACACGGG GACTCAGCAG 100
5 AGGGGCAAGA CACGACCTTT AGTTTCCCCC TTGCGATAAN CTCNC 146

(2) INFORMATION FOR SEQ ID :550:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :550:

AAATATNGAN TATCCATCCC CTCAAGCATT TATCCTTTGT GTTACAAACA 50
20 ATCCAATTAT ACTCTTTCAG TTATTTTAAC ATGTACAATT AAATTATTAT 100
TGACTCTAGT CACCTTGTTG TGCGAGCAAG TACTAGGTCT TATTCATTCT 150
25 TTCTAACTAT TCCAGGCCCT TTTTAATCAA GAAGGCTCCC TAGACCAAAA 200
TTTTAAAAAG ACAATGCTAG G 221

(2) INFORMATION FOR SEQ ID :551:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :551:

AAACATCGTT TATTCATCCA GCAGTGTGTC TCAGCTCCTA CCTCTGTGCC 50

287

AGGGCAGCAT TTTCATATCC AAGATCAATT CCCTCTCTCA GCACAGCCTG 100
GGGAGGGGGT CATTGT 116

5 (2) INFORMATION FOR SEQ ID :552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :552:

CTCATCCTCT CCTATTACAT AGTGAAGCCC ATGNCAAATA GGAAGAAGCT 50
CAGTATCGCT CCTCCACCA TAACCCCCCT TAATGCCTCC TGAACCATAG 100
20 TTNCCTCCAC TATATATCCC CCCATGTTCC TGCTACCCCA AGTTTTCACT 150

(2) INFORMATION FOR SEQ ID :553:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :553:

35 ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT 50
GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG 100
GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG 150
40 NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATAT 189

288

(2) INFORMATION FOR SEQ ID :554:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :554:

ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT 50
15 GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG 100
GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG 150
NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATATG CCTGGAAC 198

20

(2) INFORMATION FOR SEQ ID :555:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :555:

CAAGCTGAGG AGCAAGGAGA GCCAGTCTGA GTCCCAAAC TGAAGAACTT 50
35 GAGTCTGATG TTCCAGGGCA GGAAGCACCC AGCACAGGAG AAAGATG 97

(2) INFORMATION FOR SEQ ID :556:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

289

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :556:

TCTGCTGTCT GTCGCAGGAG AAGGAATGTC AGAAACTTCA TCCTCTTGTT 50
GGGGAATGCA CCCTCNTGAG TAGGCTGACC CATGAGGCTG TGGGAATTGA 100
10 GTCTTAGGAC ACAGAGACCA GGGTGTGAA TTTTCTTCCC TGCCCCTAGG 150
CTGTTCAGGT CTTCTGCAG CAGTCAGGGC TGCAAGCCCT GGAAAGGCAT 200
15 CAAAAGAGGC CCAGCTCCAG GATCGTGTGT ATGCTCTCCA GCAGACAGCT 250
CTTCAAGGGT GATCTTGTT 269

20 (2) INFORMATION FOR SEQ ID :557:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :557:

ACTCCCTCAA GGTCTGCGT CTAAGCCTAC AAGAAAGTTT GCCTATCTGG 50
ACCCTGNCTC ACGAGGTTGG CTGGAAGTAC CAGGCAGTGA CAGCCACCCT 100
35 GGAGGAGAAG AGGAAAGAGA AAGCCAAGAT CCACTACCGG AAGAAGAAAC 150
AGCTCATGAG GCTACGAAAC AGGCCGAGAA GAACGTGGAG AAGAAAATTG 200
ACAAATACAA AGGTTCTCAA GACCCACNNA CTCCTAGNTT NAGCC 245

40

(2) INFORMATION FOR SEQ ID :558:

290

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :558:

10

GAATTTAAAA AAAAAGAAAG AAAGAAAGAA AGGTTCCATC TTAGATTCTC 50

ACAACCTTCG TTCCGCAGTT CATTAATCCG ACTCTGATGC TAAGGTGACA 100

15

GTGTATGTAA GTAGATTTTT GTTTTCAGTG AAGGAGACCT GGGAAAAGAT 150

GGATTTCTCT CTGTATCTTA AGAGTTATCA GAT 183

(2) INFORMATION FOR SEQ ID :559:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :559:

30

GTCATCTTTG GAAAGTGAGA TAACCAAGGA AATAATCGAA GGAGTTAGGG 50

AGATGATTAC GTGATAATGA CTTTGGGCGC TTAACCTTTG ATCCCGGGTA 100

35

TGCTNAAGAA GCTGAC 116

(2) INFORMATION FOR SEQ ID :560:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

291

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :560:

CCTTGATGAT ACCATTATCC TCATTATAGA TGATGCACGG GCCCCTGCGC 50
TGGATACGGC GACGGTTTCT CATTTGCCTT TGTCAGCTCT CATTCGCTGA 100
10 GAGGCATAGA CCTTTTGTAT ATCATCAGGC TTTCCGTTTT TAGGAGCAAA 150
ACAGCTTCTT 160

15 (2) INFORMATION FOR SEQ ID :561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :561:

GCAGTTGGCA GGTGCACTAT CCCAGATGGG CCACTAATAG AAAGTTCCGC 50
AAATGCACCC CGTTCCCCTG TGCAGATCG TTTGAATNAG ACCAGAACT 100
30 G 101

(2) INFORMATION FOR SEQ ID :562:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

292

(xi) SEQUENCE DESCRIPTION: SEQ ID :562:

ATAAGTTATA GCAAATACAG TCTTCACAGA TTTGAGTAAC TTTATTGCAT 50
5 TTTATAGTGA TTTCTTAAGG CCTATATCCA ATGAAACCAT TTCCAAGCTC 100
TATGAGGAGT GGAATTTTAG ATGTCTATTA CATNGTCTT TTAAAAGAAA 150
AATGCTTAAC NNCTAGAATG AGCAAGATTA CTT 183

10

(2) INFORMATION FOR SEQ ID :563:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :563:

AGAGACACGT GAAATTCATA TCTCAAANNC ACAGAGCTGA GACTTTGGGC 50
25 CTAAATACTG TACCACTGGT TCCCTGAACC AAGGAAGAAA AGTGTCGGTA 100
AAGGCCCGTT AAGACAAGAT GGCAAGGAAA AGCACCTTAA ACAATGGTAA 150
GATTTATGTT AGATCAGTGG TAAGAGTTTC TAGTGAC 187

30

(2) INFORMATION FOR SEQ ID :564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :564:

293

GGGACCCCAA ATCACATCCA GAATACTAGA GTGAGGCAGC TGCAACATGA 50
CACAGAAAAA TGGAATCAGG ATTTAGGGGA ATTGGATTTC AGTGCCTATT 100
5 GAGACACGAT CTAGGAAGCC TACCACTTTG GCTGCTCACT GTATGCACAC 150
AACCCNANNA NAATNGATGA AAACAAGAAT GTACAGCATG CTCCTAACAC 200
AANGTGACTA TTC 213

10

(2) INFORMATION FOR SEQ ID :565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :565:

TCCATCTGAC ATCGCATTTT CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50
25 GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTGATGC TATCCCCCAG 100
CCCAATACAA AATACACAGA AAAAGCAATT ATTAAATAC TGGCTTCGGT 150
TTCTTTTTTT CCTTTAA 167

30

(2) INFORMATION FOR SEQ ID :566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :566:

294

GAAGATACAG AACCATCCGT GAAAATCATT TAGCACTGGA GACCTTCTTT 50
GTATTACTTC CTNGTTACTA GACCTCTAA TTCAATGGGG CCCTGCTGGT 100
5 TTGTCGATGA ATTGAGCAAC TGAGAACG 128

(2) INFORMATION FOR SEQ ID :567:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :567:

GGAGGCTCGG GAGTAGCATC CTCAGGAGTA GTGTAGCGAG CAAATTTGGA 50
20 AAGTAGTCCT CAATCTTCGA TTTCCAGCA AGGACTTTCT CAGCNAGCGA 100
TCTCGNTTGT TGAGGAACGG ATCAAGAGAT GNNNGTNTAG CTGTNNTGTT 150
25 GTTTAGATGT CTTGAAGAGG TTAGAGCCTC CTGTAGGCGG TTGGNNTGGG 200
NG 202

(2) INFORMATION FOR SEQ ID :568:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :568:

ATGTCATGAT GCCTAACTCA TACACTCTTT GCCTCAAATA TAATTACTAA 50

295

AAACAAATAT AGTATAAACA TTAAACAAAT GAACAATAAT CATCAATAGA 100
CGGGTTACTT TCAAGGAAGA GTTGTTTTGT GACAAATTCT ACTCTTGATC 150
5 TA 152

(2) INFORMATION FOR SEQ ID :569:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :569:

CAGGTCCGCG TGCTCTCCGC ACCACCCAC TTCATTCCGG CCAAACCAAC 50
20 CGCACCCCTG AATTCTCCG CAAATTTCCT GCCGCAAGG TCCCAGCATT 100
TGAGGGGATG ATGGATTCTG TGTGTTTGAG AGCAACGCCA TTGCCTATTA 150
25 CGCGAGCAAT GAGGAGCTGC GGGGAAGTAC T 181

(2) INFORMATION FOR SEQ ID :570:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :570:

ATCCCTGGG AGTTTATTCT CCTGGTAAGC TGTAATTGCA TATCCAGTTT 50
40 AACTGGACTG GGCTGTGTTG GGCGAGGATC NGCAGGGTTT TTTCCNNT 100

296

NGAAAGATGA AATAGATTNT TGAGCACTGG NTGCAGAGCC AAAATGCNTA 150
ATGCTTT 157

5 (2) INFORMATION FOR SEQ ID :571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :571:

GGCACTAAAG CCTTTAATAA TACGAGATGA AATGCAACNG TGNNATGACA 50
AGTAAGTGAG CCTGACCTGG CATTGCCTCG CCTCACCGCT GGCTTTGACC 100
20 AGGGTATGAT CTTTAACTTT TCTGAGCTGA TTTGATCGTG GTCTTTACAC 150
ACAGGTGGTC GTTCCTGTTT GGACACTGTT TTATTTGTTT GAC 193

25 (2) INFORMATION FOR SEQ ID :572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :572:

TCGCAGGAGA AAGAGGTTTT CAGAGGCCCT GAGGACATGG CTGCCCTTGA 50
GAAGGATTG AGGAGGTTGG TGAATTGTG TGAAGGAGAG GGCGAGGAAG 100
40 AAGGAGAGGA TACTAAAGTT AAAACGTCAC AAGGTGTGCT TTTAAGGGAG 150

297

CTTTCCTGTT TTAAACATGA AAGTGTTGGC

179

(2) INFORMATION FOR SEQ ID :573:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :573:

15 AGGACCTCTA AGACATCCTT ATGACGACAG TTTTGTCCAA GGGGATATCC 50
ACAGAGTACC TTGTGGCATT AGGTGATTGT AGTCATACAC TTAAAAAGA 100
TTTTATTTCT GATCTTTTGG CGATCTTCTT CTGCCCATG NNGCTGTTAC 150
20 TTNGCNCGGG NAGCGGTAA TTCTANCCGC TAGGTGTGC 189

(2) INFORMATION FOR SEQ ID :574:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :574:

35 GTGCCTTCTA GGTTTTGAAC TTCTATGCAT TAGCGCAGAT GTGGAATGCG 50
TAAAGGTGTT CATAGTTTGA CTGTTTCTAT GATGTTTTTT CAAAGAATCG 100
TCCTTTTTTG AACTATAATN CCCCNCGGTT ATTTTACCAT CACAGTTTAA 150
40 ATGTATATCT TTTACGTCTC TACTCAGACC ATATTNAAA GGGGCGCCTC 200

298

ATTATGGGGC AGAGAACCTT TTAATAAGTC TCATTAGAT CTGAATTTG 250
GTTCTAAGCA TT 262

5 (2) INFORMATION FOR SEQ ID :575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :575:

CCAAGGAACC ATCTGCGCCG CAAGCCAGAC CCCACAAGAC CTAGNTTGGT 50
CCTGAC 56

20

(2) INFORMATION FOR SEQ ID :576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :576:

GCGAGTCTCA AAGAGTAGAG GAGCGTCTAC TATCTTTCAA CTCCGATCTT 50
CTGATGNCGG ACTTTACCGT GACAGCGAAG TGGTATTGTA CGTCCAGGCC 100
CGCCAGCCAC TGTCTTCATG CAGGAACCAC AGTGCCAGAT CCCCACAGCT 150
CGTATCTT 158

40

(2) INFORMATION FOR SEQ ID :577:

299

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :577:

10

GGACCTTGAC CCACATCCAT GTTGAGGAAT GTCCTCTTGT CAAGGTCAGG 50
GAACAGCACC CACAGAGGGC CTCTGGGTCC CTCTCTGCTC AACTCCCTCT 100
CTCTCGGTTC CTGCGAGGCT CATAGGGTGC AGGGCCCAGC AGAAGGACTG 150
AGTCTTCCTC CTGGACTTCT GGTCTGGTA GGCTGTGCTT CATGCTCTCC 200
TGTCACCTGT ACTGTAAGGA ACTATTATGA CAAACGCATA AAGAATATGA 250
CTTTG 255

20

(2) INFORMATION FOR SEQ ID :578:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :578:

35

GAGGAGTCCA TGCCATCCTT GATGGAAAAG AACTGAAGA GAAAAGACAG 50
CCTGTGGAAG AAGCTCAAAG GTTCTTTGAA GAAGAAGAGA GAAAATATGA 100
CATGATATCT TTGCTTTTGA GTTCCTCAGC CTCTCTGAAT TTATTAGTTG 150
GACAATTCCA TATGCAGCAT TCTGCTTCAA TATANCTCTT NNGGTCTCTC 200

40

300

TCTCTNNAAT ATTTGCCTGT AGGTAAAAGC AAGCTCTGCA TATCTGTACC 250

TCTTGAGATA GTTTTGTTTT 270

5 (2) INFORMATION FOR SEQ ID :579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :579:

GAGTTTTCAG AGGCCCCGTA GGACATGGCT GCCCTTGAGA AGGATTATGA 50

GGAGGTTGGG TGGATCTGTT GAAGGAGAGG GNAGAAGAGG AGAGGAATGC 100

20 TAAAGTTAAA ACGTAATAAA GATGCTGCTC TTACGGAAG 139

(2) INFORMATION FOR SEQ ID :580:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :580:

35 GGCAGGAATA CATATAGTCA TCATTGCCAG ACTTAATATG AGAGGTGAAA 50

TGTTGATCC AATTATTTC TTGGATAAGT TTTTCTTTCC TATNCCTNTN 100

GTTTGATAA TATAATAAAG AAGATGAGGG GCCCA A TATAGAGCTC 150

40 CTGAGNGAGT TTTNGGAG 168

301

(2) INFORMATION FOR SEQ ID :581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :581:

CGGAGGGCCC TGTTCGGGAA AAATAGGATT TTAAAAATAT GGTTCATTAA 50

TTTAGGTTTT CTAACATCTA CTGGGGATG TAGCCTCCAG TGAGGTCAGT 100

TAAGTGGGAC AGAAACGGCA GAGGGAAGAG GTCTTTGCTT CCCCTGGGCC 150

CATTCTCCCT GGCTGCCAGC CCTTGAAGTC AGAACACCAT GGGAAAATTC 200

AGGAGTCGGC ACTGTAGCCG TCAAGTGGCG CTACTTTCCA CA 242

(2) INFORMATION FOR SEQ ID :582:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :582:

GCATTTTCT TGTGTGCTGT TTATAATAGC AAAGCAG 37

(2) INFORMATION FOR SEQ ID :583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

302

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :583:

GGAACAAAGA AAATGTACAG AGTTATATGC GCTTTTTTTT GGTATGGGGG 50
ACAAGAAACA CTTACCAACA AAAATATTTC AACAACCCCA AAATAACTTA 100
10 CTCACAAATA TGCAAAATTA TCTATGGCAT AGTATTTTCG ACTCGATGAC 150
ATTTAGAGAT AAAAAATCAA ATGGAGCTT 179

15 (2) INFORMATION FOR SEQ ID :584:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :584:

AACTGCCATG AAGTAACCTG AAGGAGGCGC TGA CTGGAGG GATTGATTAC 50
AGGATCGGAA CACTCCACAC TCGCCATTCT CTGCATATAC CGGTTAGCGA 100
30 GCGGAGCCTG GCGCTCTTCT TCGCGCTGAG CTAAAGCTAC ACACAATGCT 150
TTGCGACCAC AATNCACCCT TCATTTCGTA ACTGCT 186

35 (2) INFORMATION FOR SEQ ID :585:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :585:

5 ACCCACGGTA CTTACATCCT ATGATATGGC CTGCAAACTA AACTACAAAC 50
GCACTCACAT CGCTATAATC CTTTAAAGGA CTTAACTTT ACTCCATTAA 100
GACTTTTATG ACTTCTAACA ACCTCGCCAA CCTCCTCACC CCCCCTATA 150
10 CCTCGGAGAA CTTTCGCGTA ATAACCACGT 180

(2) INFORMATION FOR SEQ ID :586:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :586:

ACCGACATCA CGANNGACTT GGTCTTAGTT GAGCAATTG GCTAANNNNN 50
25 NTNCTNNTTA GCACGTTCTG AGTCTGTGGG ATAGCTGCCA TGAAGTAACC 100
TGAAGGAGGT GCTGGCTGGT AGGGGTTGAT TACAGGGTTG GGAACACTCG 150
30 AGANTGGCAT CCTGCATATA CTGGTTAGTG AGG 183

(2) INFORMATION FOR SEQ ID :587:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :587:

304

5 AGGTCAAGTC TACAGCTGGA GACACCCACT TGGGNGNANG AAGATTTTGN 50
 ACAACCGAAT NGTCAACCAT TTTAATTGCT GAGTTTAAGC GCACNTTAAA 100
 GAAGGACATC AGNGAGAACA AGAGAGCTGT AAGACGCCTC CNTACTGCTT 150
 GTGAACGTGC TAAGCGTACC CTCTCTTCCA GCACCCAGGN CAGTATTNAG 200
 NTCGNTCTNT CTATGAAGGA ATCGACTCTN TACTCCATAC CNNNCCGATT 250
 10 GAGACTGATG TGACNTTCCT GGGACTGNCA 280

(2) INFORMATION FOR SEQ ID :588:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :588:

25 GGTGAAGAAA CTCCAGATAT CAAGGAATTG GGAAATCCTG GGCCAAACCA 50
 CCCCAAGATG ATTAACTGA AATGTAGTAT TAGTACTNCT GCCAGATCTC 100
 TTTTAAACAT CATGTGCGTC TCTTGGGATC CAGCAAAGT GTTAAGCCAC 150
 30 AATGCCCTTG TGCCTTTTAA TATACCACAG TGCCAGTTAA ACTAATATTT 200
 TTTTTGTTG CTTTTTGGG TATTTTCATT AGTATTTTCA CAAATCTCAT 250
 35 GATAAAGGNC AAGGNCAGA ACTNCAGAGN ACTGAGCAGA GAGGCTNGTG 300
 ATGAAANGTG AAGGCTTCNA CTGACTTTAN GCAGTGGCAG TCANGNTACT 350
 GNGNNGCANG CTTANCTATG A 371

40

(2) INFORMATION FOR SEQ ID :589:

305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :589:

10

GAGAGAGAAC ACTCCCCTCC ATCCCAGCAC TATGCACAGT TCACGGCTCA 50
TATGCAAAGT GGAAGACACG TGGGACAAGA GCAAAGCACA AGTGACACAT 100
GGTCCCTCTC TAACACCTCA GCACACCAAC CCTGACGCTC CCATCACAGA 150
TGCTGNTCAT TCTTNCACGG NCCCCTTTTA TAAT 184

15

(2) INFORMATION FOR SEQ ID :590:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :590:

30

GGGGGCCCCG CGTNACNCC CCCACACTCT TGGTAGGCAA TGCTTGTCCT 50
NATATAGTTG NNGTCCTATC GAGTGACACT CTCGTTTCATG GATANGGTGN 100
GTAAAACCCN TNGTNGCATC CNNATTGGGN GCANTGNGCC TNTCCCCTTN 150
AANGGTTTTT GCNTNCACTC GACCTNGGGA GGATTCAATG NACNNNCTNG 200
CANTGGNCAA GCNTTGNTTG CNNGNATTGA GAACCCNCCA ATT 243

40

(2) INFORMATION FOR SEQ ID :591:

306

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :591:

10

ATTGCCCCNN TAAGTAAGTC GTNATTANAC GCGACGNCTA CTA CTGAGAC 50
NCGCATGCGC TCTCTCTACA CTAAAGCTCG TCGCTNGNTN ACTTGCGNGN 100
NAAAAAACC CCCTGGGNNC GCTTTTCACC CCCAACTTT CAAATTCCGC 150
CCCTTTNGGC NANGCCCAAC CANNCCCCC CCCTTTTNC CGNCCCANNC 200
TTNGGNCNTA ANNATTNAGN CGGNANGNNN GGGCCCCCGG CCAACCC 247

20

(2) INFORMATION FOR SEQ ID :592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :592:

35

GGAGGGGAGT AGAGGAAATT TTCATTCTGG AAAAAATGC ATACTGTTTG 50
ATATATTACT CNTCATGCTT TCCACAGATA TTATACACAG ATATTATATT 100
CCANGGATTA CGTTGCAATG TCTTCAAAA TAGANAATTC ATTTTATATT 150
TCTNGATGAA ATATAATAGT ANCTNNGCTA CTTTGGGAA TGTGACAAA 200
TACTATGATG ATTACAACTC ATTAAAGCAT AAATNTGCAT GATTAACTN 250

40

307

CATGTTCCCTT CTATGANCTN CGTGGNATAT AGGCATATTT ATTAATGCTA 300
TTTANGGCNT NNGTGCTTTG TAATGATTCTG NCNTTAGGTG AAGGGNTACT 350
5 TTTNTNNTNC TTCNTAGTAG ATTNNGTTNN NTCTTTTAA GAGGANTCNA 400
NTTTCATGNG TAANCATCAT CTTTT 425

(2) INFORMATION FOR SEQ ID :593:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :593:

20

CGCTGCATGC GTCAGCGCNA CGCGACGACA GCGCGCGCGA CGCGCGCGAC 50
GCACAAAANA AATGCATGCC AACACGAANA TATGTGCACA CAAACGCAAA 100
25 CGCGTGTAAC CACATGCGCG CNNGCGGCNC GCGATNCAA GCTGAAATGT 150
GCNNGNCNGT CGTGNGCGNA AATGTGAAAT GAACAAACAA CAATGAATGA 200
ATGAATGTGA AAAAGAGNGN GNTTGAAAAT TNTANAGNNC CCCCCCNTNA 250
30 ANCAAAAAG 258

(2) INFORMATION FOR SEQ ID :594:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

308

(xi) SEQUENCE DESCRIPTION: SEQ ID :594:

	GACCCTAACA ATATGTACAA AAATATAAAA TGTAATAAAA AAATACAAAC	50
5	AAATTCCTT TTAAAGTAC TTTAAGAAA AAAAGCAGGG CCTTGGAGT	100
	TTGGTTCTT TTTCTCTCC CTGTTGCAAA TTCTCATGGT TTGGGTGGG	150
	TGGTGGAGAG CGCGTGTCAT CTGCGGTGC CTGCCACGT GGGCGGGCGG	200
10	CTCTCTACTC GAAGG	215

(2) INFORMATION FOR SEQ ID :595:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 272 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :595:

25	GGGGCTGGT TGGTCATCCG AGATCATTAA AAATGGCTGA CCCTAACAAT	50
	ATGTACAAAA ATATAAATG TAAATAAAAA ATACAAACAA ATTCCTTTT	100
	TAAAGTACTT TTAAGAAAAA AAGCAGGGCC TTGGAAGTTT TGGTTCTTTT	150
30	TTCTCCCCT GTTGCAAATT CTCATGTTTT GGGTTGGGTG GTGGAGAGCG	200
	CGTGTCATCT GCGGGTGGCA CTGCCACGGT GGGCGGGCGG GCTCTCTACT	250
35	CGAAGGTGAC CACGTTTAGA TT	272

(2) INFORMATION FOR SEQ ID :596:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 250 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

309

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :596:

GACAAACTGT TGACACCCGG AGGCCTAAAC GAGGATTTCA GCTTCCATTA 50
TGCCCAACTC CAGTCCAACA TCATTGAGGC GATTAATGAG CTGCTAGTGG 100
10 AGCTGGAAGG GACAATGGAG AACATTGCAG CCCAGGCTCT GGAGCACATT 150
CACTCCAATG AGGTGATCAT GACCATTGGC TTCTCCCGAA CAGTAGAGGC 200
15 CTTCTCAAA GAGGCTGCCC GAAAGAGGAA ATTCCATGTC ATTGTAGCAG 250

(2) INFORMATION FOR SEQ ID :597:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :597:

CTGCCAAATA CTTTCTTCAC CAACTCATGA GGAGAGGGAA CATGCTGAGA 50
30 AACTGATGAA GCTGCAGAAC CAACGAGGTG GCCGAATCTT CCTTCAGGAT 100
ATCAAGAAAC CAGACTGTGA TGA CTGGGAG AGCGGGCTGA ATGCAATGAG 150
35 TGTGCATTAC ATTTGAAAA GATGTGAATC AGTCACTACT GGAAGTGCAC 200
AAACTGGCCA CTGACAAAAA TGACC 225

(2) INFORMATION FOR SEQ ID :598:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs

310

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :598:

ACAAAACGCA GATATAAAAA AGTTACAAAG ATTTTATAGAT TTTCATTCAC 50
10 AAAAAAAGTC ATTCACATTT TACACTATAC ACGTTATGAT ATAATACAGG 100
AAAGTATTAT GTGCATTGTA AGAGAAGGAA AATAGAACTA CTAGATCACA 150
15 CGTGTGTGTTT TGTGCTCTAA AATACCTAAA GGTGGATTCA TTTAATGCAA 200
CACCAGGGAC 210

(2) INFORMATION FOR SEQ ID :599:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 116 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :599:

30

AAAGGAGTTG AGTACTGTAA ACGCAGAGCT ACATAGAAAA AACGGGCTTC 50
AAAAATCTGC ACAGAGGTTT GCTTGAGAAT TTAGCTACAC AAATATGTGT 100
35 AGAAGTGAAA AAAAAA 116

(2) INFORMATION FOR SEQ ID :600:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

311

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :600:

ACAGTGTGTG CCCTGTCAGC TCCGCAAATT GGCAGTCACT ACGTTTGTGC 50
CCCCGTGAAC CTTGTGATCT TCACTGCCAC TAGCGATGAA GTCTTCATTA 100
TGGCCTC 107

(2) INFORMATION FOR SEQ ID :601:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :601:

ACTGCTAGTG AAATTCACAT GACTCACAAAT TCCCTTTAGC CAATGTTACC 50
GAAGTCAGTG TCAAGAAAAC TTAACAGAAA AAAAAAGCA CAGAGTGAGT 100
TCCTACCATA AAAATCCAGG CTGCCCTGTT TCCTAGCTCT AATATAAGCC 150
ATTTTCTTTC CTTAGTGTA CAA 173

(2) INFORMATION FOR SEQ ID :602:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

312

(xi) SEQUENCE DESCRIPTION: SEQ ID :602:

5 GGAAGAGAAC ACATACACGA GGACCACTAC CTGATGAGGA CAAGAGAGAT 50
GGGAANNNGC TGTGGAATTC CTTTCGGCAC CCTGGATGTT AACCCCTGCT 100
CAGGAAAGGG TGCATCTGTC TTCATCATGC CTCTCTCTCC TCCTCCTCCA 150
GCCACCTCCC AAAGGCAGAG CTGCCGCAAC CTGCCTGGCC ATGTGGTGGC 200
10 AAGTACCCAG TAGGAG 216

(2) INFORMATION FOR SEQ ID :603:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :603:

25 GAAAAAACA TCATGACAGC AACTCTCCTA ACCACAAAA TCACATATGT 50
TATCTTTCTT TCAGGACTAA TAATTAATAT TTAAGAGGAA AGCACATCAA 100
TTTCTAGGGC CCTTCTTGGG GAAAGGTTCA TATAATTTAG CATACATACA 150
30 TATTCAGTGA ATGCATTCAT ATATTACTAT ATAAACACTC TCAGCTACAA 200
TGGTAATATA ATG 213

(2) INFORMATION FOR SEQ ID :604:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :604:

5 GACATCTGAT CATCTCACTG GACGCCACAG GGGCAAGAGG GTGGTTTTCC 50
TGAAGCAGCT GGCTAGTGGC TTATTACTTG TGACTGGACC TCTGGTCTCA 100
ATCGAGTTCC TCTACGAGAA CACACCAGAA ATTTGTCATT GCCACTTCAA 150
10 CAAAATCGAT ATCAGCAATG TAAAAATCCC AAACATCTTA CTGATGCTTA 200
CTTCAAGAAG AAGAGCTGC 219

(2) INFORMATION FOR SEQ ID :605:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :605:

25 AGCGAACACG AGCACAGCGA GCGCACAGAG AGCAGCAGGG AGGGCAGCCA 50
CCGCCGGGAC GCCGGCAGGG GCACGAGAAG GCAAGGAGCG GACACCCGNG 100
30 NNGA 104

(2) INFORMATION FOR SEQ ID :606:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :606:

314

5 AATAAAGCAT TCTCACAACC TTTGTTGGGT CAATGATTCC TTTTACCAC 50
ANNTACAGAA TCTCCACCAT AGCATCA...A CCAACTCTGA GGAACCTCGC 100
ATAATTCTTA ACTACAAAGA TCCTTCAACA CCCGCATTCT TACAATGTCA 150
TCGCCGGAAT TTTGAGTGTT CTTTCAATAA CCTACANTA 189

(2) INFORMATION FOR SEQ ID :607:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :607:

20

GGAAAAGNTC ATTACATAAG CACCAAGNCA TTGATTATGA TCCACCGGAA 50
GAGCTCGTAT TTATCCTTTG CTTTATNTG AGACCAAGCT AGCCCTGAGT 100
AATTTTANNT GGTTCTTAAA ACATATGGCT TATCGTACTC TAAGAAAAAT 150
GCCTTACGCA CATTCTTTN T 171

25

(2) INFORMATION FOR SEQ ID :608:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :608:

40

GGAAAAGTNC GCATATAGCG TGCNATAATA CTACGNCTAA GGAGAAACAA 50

315

TTTCCTACAC ATAAAGTAGT GAGAACATCA TCCTATAACA GGGAAGTGTG 100
ATTATTTAAA AAACGCAGAA CTTATTTATT TGGCTTTAGA AATAACTGCA 150
TACAATGTCA TAAGTCGAAA AGAACTCAAA ATAA 184

(2) INFORMATION FOR SEQ ID :609:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :609:

GGGGACAGCT NNNNNGTTGT TTTGGAGCCT GTTGACTTG TATTCTCTGC 50
CTGTGATTTT CNNTTCTAAA TGAAACTCCA TGTNNNAACC AGGACGAAGN 100
TGAGAAGGAA AACGCCAAAT GCTTTGGTTA TTAGAGNTTA ATAGGNAAGC 150
TCTGTTACAC TAGGTGTAGA GTTCCAGAAT GTTCTTTTGT T 191

(2) INFORMATION FOR SEQ ID :610:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :610:

GCAACTGTGC AAACATCCAT CAGTGTGGAG GAATGGTAAA CTGGGTACAT 50
GCATGCANTN GNNNCATATT TTTGTGGTTA AGATNNTGAT GTATAGGCAT 100

316

GGAATGTTAT CAAAAGCACA TTAAGTGGTC AAAGCCAGAT ACAGAAGAGT

150

AGGTATGATT TTATAGGNAT AA

172

5 (2) INFORMATION FOR SEQ ID :611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :611:

TCCACCTTAC AGACCTGATT TGGCTGCTTC TGACGTCTGT TTCCTAATCT

50

T

51

20

(2) INFORMATION FOR SEQ ID :612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :612:

CGCCTGAAAC TTTGAGGATA AACTTTTCA AAAAAATAAA ACAGTATCTC

50

35

TTAATCACTG

60

(2) INFORMATION FOR SEQ ID :613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs

40 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

317

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :613:

TTGAAGCTGG GAGGCAGAGG TTGCAGCGTG CAGAGTCGTG CCACTGCACT 50

CCTGGGCGCA CAGCGAGACT GTCTC 75

10

(2) INFORMATION FOR SEQ ID :614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :614:

ACGGGATTCT CTTCTTCGGC CGCCA 25

25

(2) INFORMATION FOR SEQ ID :615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :615:

GCAGTGTA CT ATGTTCCGAT CTGTGAATAG CCACTGCACT CTAGCCTGGA 50

TAATATAGTG AGAACCCATC TC 72

40

(2) INFORMATION FOR SEQ ID :616:

318

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :616:

10

TCTAACTGAT TTCAAAGCAA ACTCTCTCTT AATTAGGCTG CCTCTCCAGG

50

GGAAATTTAG TGGCAGGGTC CCAGTGAGCC TGTAAGAAGT GTTCTACTCA

100

15

CCAGAGTCAC TACTCCAGGT TGAGGACATG AGGCAGG

137

(2) INFORMATION FOR SEQ ID :617:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :617:

GCAGGGCAGT CTTGGTGTGC AGCCCTCTC CTCTCTGTCC CCTGACACTC

50

30

CACAGTGTGC CTGCAACCCA AGTGGCCTTA TCCGTGCAGT GGTGGCAGTT

100

CAGAAATAAA GGGCCCATTT GAGGGATGAC CGCATTAC

139

35

(2) INFORMATION FOR SEQ ID :618:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :618:

5 TCTTCTTACT ACACTGGAAG TCTGAACTGG GTGCCTGTTA CCGTCGAGGG 50
TTACTGGCAG ATCACCGTGG ACAGCATCAC CATGAACGGA GAGGCCATCG 100
CCTNCNCTGA GGNCNGCCAG GCCATTGTTG ACACCNNCAC CTCTCNCTG 150
10 ANNNNCCCAA CCAGCCCCAT TNCCAACA 178

(2) INFORMATION FOR SEQ ID :619:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :619:

ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC 50
25 TTCTGCGGCC GCCACGCGT GGA 73

(2) INFORMATION FOR SEQ ID :620:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :620:

40 TGCCTTACAC ACTCAGGGAG ACCTCGGGTT GTACCTAGGC CTAGTGGACA 50
AACTTTGGTA GAGGGTTCGG TACGACTTAC GACACCTGGC CCTACGTCAT 100

320

AGTCCGTACC CTCAGTAACA GTGTAGTAGC TCTTCCTGT

139

(2) INFORMATION FOR SEQ ID :621:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :621:

15 TTCAAAAACA ACTTTATTCA TGACACATAT TAANNNAACA CCCCACCCCT 50
GGAAATGAGC TAAAAAATA AACAAATCC ACCTCCCACC TCCCTGNNCC 100
CACTTCCTCC CATGCCCTCC AAA 123

20

(2) INFORMATION FOR SEQ ID :622:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :622:

35 CACCCAAGAC CATCCTTTAT TGTAGTATTA GTTCATGGTA ACTGCATGAA 50
AAAACATTTC NNGAGGAATT TTCAATTTC AGCTTAAAGA ACNNNCCCAC 100
CAACATAACC AATTTATGAA ANNNAATTCA TTAAAAGGTA TAGAACCTCT 150
TGTNNNCATG ATGGCAAGGG ACA 173

40

(2) INFORMATION FOR SEQ ID :623:

321

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :623:

10

TTTATTGTAT CATGAGGCAT TGAAACATCT GAATAAATCA ATGTCTGGGC 50

GGTGAAGGCA GCTGCTTTCT CCTTCACTTC TTTGGGTAC TAGAGCAACT 100

15

TGTCAGTAGA TT 112

(2) INFORMATION FOR SEQ ID :624:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :624:

ACTCCTTCTG CCCCCGTTCT TCTAGTGAGA GGGGCGGACA AGGGGGCGGC 50

30

GAAAAGAGGA GAAAGGAGAG AAACAAGAGT CGAGGGGGAC AGGGGAGTCG 100

AGGTCTGCAT CCCCTCCCC 119

35

(2) INFORMATION FOR SEQ ID :625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :625:

AACAGCACGG AGATTGCGTT TATATATCAG ACCAAGCTC

39

5

(2) INFORMATION FOR SEQ ID :626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :626:

CCAGCGCCGA GGTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA

50

20

ATAAAAATCT GAAAACATCC CC

72

(2) INFORMATION FOR SEQ ID :627:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :627:

CCTCCGCCGG AGCTATCTGC ACTACATCCG CAAGTACAAC CGTCTTCGAG

50

35

AAGCGCCACA AGAACATGTC TGTACACCTG TCCCCCTGCT TCAGGGACGT

100

CCAGATCGGT GACATCGTCA CAGTGGGCGA GTGCGGCCTC TAGACAAGAC

150

40

AGT

153

(2) INFORMATION FOR SEQ ID :628:

323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :628:

10

AAAAGAAGTA GGTCGTGTCG TTCTGGTTGC CCTAAGAGAA GAAGANNNCG 50
GTGGCCACCT CGAGGTTAAG AGGGATATCA CTCAGCATAA TGTTAAGTGA 100
CCGGCAGC 108

15

(2) INFORMATION FOR SEQ ID :629:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :629:

30

TCGCACCACT AGAAANCACC GTGACTGAGA AGAATGATGT GACCTTCAGA 50
CTTGACCCNN GGACAATGNC AGCTCCCAAT GNCCGTCTAG TGGCA 95

(2) INFORMATION FOR SEQ ID :630:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

324

(xi) SEQUENCE DESCRIPTION: SEQ ID :630:

CCAGCNCCGA AAAGCCAAGA CTTCAATCAAC TACATAGGTC TTACCATTGA 50
5 CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT 100
AGAAAGGCAT CTTTCGCCAG TGGATTGCC TCAAGGTTG 139

(2) INFORMATION FOR SEQ ID :631:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :631:

20

CCACCGCCCC GAGCGAATGT AACCCGGCCT TGGACGACCC GACGCCGGAC 50
TACATGAACC TGCTGGGCAT GATCTTCAGC ATGTNCNNCC TCATGCTTAA 100
25 GCTGAAGTGG TGTGCTT 117

(2) INFORMATION FOR SEQ ID :632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :632:

CCAGCNCCGA AAAGCCAAGA CTTCAATCAAC TACATAGGTC TTACCATTGA 50
40 CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT 100

325

AGAAAGGCAT CTTTCGCCAG TGGATTGCC TCAAGGTTGA GGCCGCCATT 150
GGAAGATGAA A 161

5 (2) INFORMATION FOR SEQ ID :633:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :633:

CCTGCNCCGA CGATGCCAG AATCCAGAAC TTTGTCTATC ACTCTCCCCA 50
ACAACCTAGA TGTGAAAACA GAATAAACTT CACCCAGAAA AACAAAC 97

20

(2) INFORMATION FOR SEQ ID :634:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :634:

CCAGCNCCGA AGCATTGGAT GCTTGACAAA CTAACGGGTG TATTGCACC 50
TCGTCCATCG ACAGGTCCCC AGAAGCTGAG GGAATGTCTT TCCTCTGATC 100
TTCTTCCTCA GGAATAGACT CAAGTATGCG TTGACTGGAG ATGAGGTAAA 150
GAAGATATGT ATGCAACGTT CATTCAAA 178

40

(2) INFORMATION FOR SEQ ID :635:

326

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :635:

10

CCTGCNCCGA TGCACCCGCC ATCCAGCCTG TCCTTTGGAC CAGGCCACCC

50

CTCCAGCATG GTCACCGCCA TGGGTTAGAN CCCTGCTCGA

90

15

(2) INFORMATION FOR SEQ ID :636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :636:

CAGGAGACAC AGACAATAGT CACTACATCA CAGCCTTGTT CTTTCCGAAG

50

GATAAAATGT CATTCAAGAA TGGGGTGAGG TGGTTAGAGG GACTAGGTAC

100

30

T

101

(2) INFORMATION FOR SEQ ID :637:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

327

(xi) SEQUENCE DESCRIPTION: SEQ ID :637:

CCGAGCACGA GACCCTGATG CACATTCTAA AATAAAAGAA TGATGCACAT 50

5 TTAATAAAG CACAGCACAA 70

(2) INFORMATION FOR SEQ ID :638:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :638:

CCGAGCANAN TCTAACCCGG CCTTGGACGA CCCGACGCCG GACTACATGA 50

20 ACCTGCTGGG CATGATCTTC AGCATGTGCG GCCTCATGCT TAAGCTGAAG 100

TGGTGTGCTT GGGTCGCTGT CTACTGCTCC TTCATCAGCT TTGCCAACTC 150

25 TCGGAGCTCG 160

(2) INFORMATION FOR SEQ ID :639:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :639:

CCGAACAAAT GTACGGAATG TGTGAGTCCC TCTGGAGCCC AACATGGATC 50

40 CGGATCACCT GTTTGAAACC ATCTCCCAAG CCATGCTGAA TGCTGTGGGC 100

328

CGGGATGCAT GTGCAGGCAT GGAGTCATTG TCACATCA

138

(2) INFORMATION FOR SEQ ID :640:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :640:

15 CCGACCACCC CTCCTTTTC TTCGTCCATC CAGCACAGCA AGACCAACGG 50

GATTCTCTTC TCGGGCCGCC ACCGCGTGGA 80

(2) INFORMATION FOR SEQ ID :641:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :641:

30

AACTAAACTG TTACCTTCCC TCGCTCCACA GAAGAAGACA GCCAGCTTCA 50

GGGGTCCCTG TTGCTGGCCA AGCCAGTGAG CCTGCTGGGA GGCTGGTCCA 100

35

(2) INFORMATION FOR SEQ ID :642:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

329

(xi) SEQUENCE DESCRIPTION: SEQ ID :642:

AGAGGACAGA AAGGAACAGA ATGATCTTCC TACNCACAAC ACAAACGTCA 50
5 GTTAATGTTC CATCCATGCT GCTTAAA 77

(2) INFORMATION FOR SEQ ID :643:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :643:

20 CCAGCGCCGA GAGCAGCCCC AGTAGCAGCN CATGGCCGGG TCCAACGCCT 50
ACATCGACAA CCTTCATGGC GGACGGGACC TGTCAGGACN GGCCATCGTG 100
GGCTACAAGG ACTCGCCCTC CGTCTGG 127

25

(2) INFORMATION FOR SEQ ID :644:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :644:

GTAGCCAGAC CACAACACCG AGTTGTACCC AGATAGCTGG GATTGGAAGT 50
40 GAGGAGGTTT CTCACCCAC AGATAACCCA AGACACAAAT GTGCAATTAA 100
AAGTTTATTT TAGACC 116

330

(2) INFORMATION FOR SEQ ID :645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :645:

CCACCACCCG ATTCGTGACC AAGAAGGCTC TGTGCATTCG GGTTTTCCAG 50
GAGACTCAAA AGCCGAAGAA GCGAAGAAGA GCCTTAAAGG CTGCAGCAGC 100
CAGAAAAACA AGCAAAGGAG GAACCCAGAC AGCCCTGCAA AGCATAAAG 150
ACACTCAAGA CAGCAATTAA TCTGTCATCA TT 182

20

(2) INFORMATION FOR SEQ ID :646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :646:

CCAGCGCCGA GGTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA 50
ATAAAAATCT GAAAAC 66

35

(2) INFORMATION FOR SEQ ID :647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

40

331

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :647:

5

CAAGACAATA GTCACATCAT CGCAGCCTTG TTCTTTCCGA AGGATAAAAT

50

GTCATTCAAG AATGGGGTGA GGTGGTTAGA GGGAGTAGGT ACT

93

10

(2) INFORMATION FOR SEQ ID :648:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 114 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :648:

CCCCTTTTG TCCCCACTGA GATGTATGAA GGTTTGGTC TCCCTGGGAG

50

25

TGGGTGGAGG CAGCCAGGGC TTACCTGTAC ACTGACTTGA GACCAGTTGA

100

AAAGTGCACA CCTT

114

30

(2) INFORMATION FOR SEQ ID :649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :649:

40

CTGCNCCGAC CACCCCTTCC TTTTCTTCAT CCAGCACAGC AAGACCAACG

50

332

GGATTCTCTT CTGCGGCCGC CACCGCGTGG A

81

(2) INFORMATION FOR SEQ ID :650:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :650:

15 AGGAGCNCCG ACAAAGACA CATTGGACCT GTCAGCTCCT CTGTTTCACC 50
AAGCAGACAC AATAACCTTA CCAACAAAGC AGAGTAAGCC AAGTGCCTCT 100
GTGTGACACC ACCGCATNNT GATGACGCAT AATAAAAATA TAACTAATTT 150
20 AGACTAGAG 159

(2) INFORMATION FOR SEQ ID :651:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :651:

35 CCGACCACCC CTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50
CTCTTCTGCG GCCGCCACCG CTGGAGCT 78

(2) INFORMATION FOR SEQ ID :652:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs

333

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :652:

CCGACAGACG GTCATTGATT ACAACGGGGA ACGCAGCTG GATGGTTTTA 50
10 AGAAATTCCT GGAGAGCGGT GGCCAGGATG GGGCAGGGGA TGATGACGAT 100
CTCGAGGACC TGAAGAAGC AGAGGAGCCA GACATGGAGG AAGACNATGA 150
15 TCAGAAAGCT GTGAAAGATG AACTGTAATA CGCAAAGCCA GACCCGGG 198

(2) INFORMATION FOR SEQ ID :653:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :653:

CCGAAAAGCC AAGACTTCAT GAACTACATA GGTCTTACCA TTGACCTAAG 50
30 ATCAATCTGA ACTATCTTAG CCCAGTCAGG GAGCTCTGCT TCCTAGAAAG 100
GCATCTTTCG CCAGTGGATT CGCCTCAAGG TTGAGGCCGC CATTGGAAGA 150
35 TGAAAAATTG CACTCCCTTG GTGTAGACAA TACCAGTTCC ATTGGTGTTG 200
TTGCTATAAT AACACTTTTC TTTT 224

(2) INFORMATION FOR SEQ ID :654:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs

334

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :654:

CCGCCTCAGA CTCTGGACCA GCCACTGTCC CAGAAGCCAG GCCGGGCAGT 50
10 GGCCTTCTCC ACTCCCCTCT GACTTCTCCA AGGGGCTCAG TGGCCAGTGC 100
CCCCCAGGAG GCTCCACCCT CAACTCAACC CAAGCAAGAG GGACAGATGA 150
15 AAAACAAAAT CCAATCAGGG CGATAAATGG CGGGGGGTTT AATTGTTT 200
CTGAGCGCAT AAAGCTAAGG AGGGGT 226

(2) INFORMATION FOR SEQ ID :655:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :655:

30

TTAAAAAAT TCCCCCTTT AATTGACCAA AGTAAAGCCA TGACATTTCA 50
TTTGGTAACC TGTTTAGAAT TATAAAATC ATTTCATTTG GCCCAGCCCA 100
35 TACGCCCAAG AGAAACTTC CAGACTTTTC TGATGCCATC CAGTTTTGTT 150
CTTACAAAAT GCATATT 167

(2) INFORMATION FOR SEQ ID :656:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

335

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :656:

CCACCCCTTC CTTTCTTCA TCCAGCACAG CAAGACCAAC GGGATTCTCT	50
TCTGCGGCCG CCACCGCGTG GA	72

10

(2) INFORMATION FOR SEQ ID :657:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :657:

AGAGGGTTTT CTATATGTAA TTCTTTTATT CTGTAAAAGG TAACAAAATA	50
TACAGAACAA AAAAATTTC CCTTTTAAA ACTAATGTTA CAAATCTGTA	100
TTATCACTTG TATATAAATA GTATATAGCT GATCATTAAT AAGGTGTATA	150
GTACAATGTA TTCTAAAACT GTTCCGCC	178

30

(2) INFORMATION FOR SEQ ID :658:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

336

(xi) SEQUENCE DESCRIPTION: SEQ ID :658:

CCGACCACCC CTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50
5 CTCTTCTGCG GCCGCCACCG CGTGGA 76

(2) INFORMATION FOR SEQ ID :659:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :659:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT 50
20 AACAAAAACC NTGAAAAC 68

(2) INFORMATION FOR SEQ ID :660:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :660:

35 CCCAACTTC TTTAAAATC AAGTAATGTT TACAAGAAAG AATAAAATCT 50
TAATCCTTTT CACTTTTAAA GACAATCAGA TAAGATTACC CACTGCGATT 100
AAACACTGAT CAAACTCAGT TGCCTTACG TTAGCATTAC TCTGTCATAG 150
40 C 151

337

(2) INFORMATION FOR SEQ ID :661:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :661:

AGGCACTGAC CCCTGCCACC CCTCACTGCA TTAACCTCAG CCACGTCTCC 50

15

TCCTTCCTCT GCGCTTCCAG TGATAAGGGT ACTGTCCATA TCTTTGCTCT 100

CAAGGATACC CGCCTCAACC GCCGCTCCGG CCTGGCTCGC GTGGGCAAGG 150

TGGGGCCTAT GATTGGGCAG TACGTGGACT CTCAGTGGAG CCTGGCGAGC 200

20

TTCCTGTGC CTGCTGAGTC AGCTTGCATC TCGCCTTCG GTGCG 245

(2) INFORMATION FOR SEQ ID :662:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :662:

35

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50

AATAAAAACM TGAAAACACC CC 72

(2) INFORMATION FOR SEQ ID :663:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

338

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :663:

10	GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTGCCTAT CACTCTCCCC	50
	AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG	88

(2) INFORMATION FOR SEQ ID :664:

- | | |
|----|-------------------------------|
| 15 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 223 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 20 | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :664:

25	GCCTGCGCCG ACAACAAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCCG	50
	GAAGTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC	100
	CCCCACCTGC TGTTCATG ACCCAGGGGG CGCACACTAC CCCACAGGCG	150
30	CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG	200
	CGGATAGTCA CACTCCCTGC CGA	223

35 (2) INFORMATION FOR SEQ ID :665:

- | | |
|----|-------------------------------|
| 40 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 70 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

339

(xi) SEQUENCE DESCRIPTION: SEQ ID :665:

5 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50
AATAAAAATC TGAAACACC 70

(2) INFORMATION FOR SEQ ID :666:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :666:

20 GCCAGCGCCG ACCGCCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50
TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAAA CCAAACCACC 100
TTTCTACGTA CCGTATAG 118

25

(2) INFORMATION FOR SEQ ID :667:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :667:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTTGCCTAT CACTCTCCCC 50
40 AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :668:

340

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :668:

10

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTTGATCTTC AACTCTGCAT 50

ACAAGCAGA 59

15

(2) INFORMATION FOR SEQ ID :669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :669:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA 50

CATGGATCCG GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100

30

CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150

GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC 200

35

CTGCTCCCAG AGCCCACTTT TTT 223

(2) INFORMATION FOR SEQ ID :670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

40

341

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :670:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC

37

(2) INFORMATION FOR SEQ ID :671:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :671:

20

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC

37

(2) INFORMATION FOR SEQ ID :672:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :672:

35

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTCGATCTTC AACTCTGCAT

50

ACAAGCAGA

59

(2) INFORMATION FOR SEQ ID :673:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

342

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :673:

GCCTGCGCCG	ANGCATTCCC	TTTGACCTGA	GTCTGCAGCA	GGTCCCTTTT	50
10	GGGCTTCCTT	CCCCTCAGGT	AGCCTCTCTC	CCCCTGGGCC	100
	ACTCCCGGGG				
	GTGAGGGGGT	TACCCCTTCC	CAGTGTTTTT	TATTTCCGTG	150
	GGGCTCACCC				
15	CAAAGTATTA	AAAGCAACTT	TGCAATT		177

(2) INFORMATION FOR SEQ ID :674:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :674:

30	GCCTGCGCCG	AGCACAAGAC	AATGACGAAC	ATTTTAAAAA	AAAAGAATGA	50
	CGCACATTTT	AATAAAGCAC	AGCACAA			77

(2) INFORMATION FOR SEQ ID :675:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

343

(xi) SEQUENCE DESCRIPTION: SEQ ID :675:

5 GCCAGCGCCG ACACCCAGAG ACTACAGTAC TTAGGGGTTA CACACAACAG 50
CCGTAAGTGG CGGCTATCTG TTCATAACAA ACAAACCATA GCATATTTAC 100
ACCGCATCAC ATCGAGTGAT TATAGAAATC CATAACACA CCGATTGCAT 150
AAAATCTTTT TTTAGGAAAA AAACAC 176

(2) INFORMATION FOR SEQ ID :676:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :676:

20 GCCAGCGCCG ACGCCAGAG AATACAGTAC TTAGGGGTTA CACACAACAG 50
25 CCGTAAGTGG CGGCTATCTG CTCATAACAA ACAAACCACA GCATATCTAT 100
ACCGTATCAC ATCGAGTGAT TATAGAAATC CACAGAGAGA C 141

(2) INFORMATION FOR SEQ ID :677:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :677:

40 CTCTGAACAG ACACGAAGCT GCCCTCGTA CAGCCACTCG GGCGCTGACC 50

344

	ACCAGGGAAG GCAAAGGCAT AGGACTTCCA CACAGTCCAG ACACTGCACG	100
	CTGACAAGCG CCTCCGCGGC GGCTGCGAGC CGGACTCAGG CGGATCTTGA	150
5	CAGCCTTGCC CGCGAGTGCC CGGGGATAGA ACCCGTGCGC GTGGACCTAG	200
	GTGACTGGGA GGCCACCAAG CAGGCACTGG GCAGCGTGGG CCCCCTGGAC	250
	CTGCTGGAGA ACAACACCAC CGTCGCCCTG CCGCAGCCCT TCCAGGAGGT	300
10	CACCAAGGAG GCCTTCGACA GATCCTTTGA GGTGAGCTTG CGTGCGATCA	350
	TCCAGGTGCT GTAGA	365

15 (2) INFORMATION FOR SEQ ID :678:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 366 base pairs
	(B) TYPE: nucleic acid
20	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :678:

	GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC	50
	CAGGGAAGGC AAAGGCATAG GACTTCTGCA CGGTCCAGAC CCATGTACGC	100
30	GACGGGCGCC TNCGCGGTGG CTGCGAGCCG GATTGAGCA GATCTTGACA	150
	GCCTTGCCCCG CGAGTGCCCCG GGGATAGAAC CCGTGTGCGT GGACCTNGGG	200
35	TGACTGGGAG GCCACCAAGC AGGCACTGGG GTAGCATGGG CCCCCTGGAC	250
	CTGCCCGGAGA ACAATACCAC CGCCGCCTNT GCCGCAGTCT TTCCCGGAGG	300
	TCACCAAGGA GGCCTNTTGA TAGATCTTTT GAGGTGAGCT TCGTGCAGT	350
40	CATCTAGGTG CTGTAG	366

345

(2) INFORMATION FOR SEQ ID :679:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :679:

GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC 50
15 CAGGGAAGGC AAAGGCATAG GCCAGCACCG ATGAATTCCC TTGACCTAA 100
GTCTGCAGCA GGCCCCTTTT GCGCTTCCTT CCCCTCAGGC AGCCTCTCTC 150
CCCCCGGGCC ACTCCCGGGG GCGAGGGGGT TACCCCTTTC CCAGTGCTTT 200
20 TTATTCCCGC GGGGCTCACC CCAAAGCATT AAAAGCAGCT TTGCAATTCC 250
TTG 253

25

(2) INFORMATION FOR SEQ ID :680:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :680:

GCCAGCGCCG AGGCTTCTCC TAGGGCTGCT CCTGGGCCTA GCTCTTACAG 50
GCTCGTCCCC CAGGCCTGCC CTTCTCCACT GCCCCCTCCC GTGCCTGGGC 100
40 CCACACACCC TTCAGGAAGG GGGAGCACTG AGAAGCACAG CACAGGGGCT 150

346

CAGCCTGGGA TCCGGTGACG GCCTAGGCAG AGGCTGGGCC AGGAGTCCCA 200
AAGGTCAGTG ACAGTTTCTC AGAAGGGGCC CAGCGTCCAC CTCTCTCCCA 250
5 GGACCAGACA CCCCTTCCAG GCTCCCCCAC CCCCTACGG GCTC 294

(2) INFORMATION FOR SEQ ID :681:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :681:

CCGCCAAGTG ACACCAAAGC CCTGGTTGAC TTTGACAGCC CCGTGGGGCG 50
20 GCGGGAGGCC GGGCACTCTA GGGTCTACCT ACCAGTGCAA TCGTTTAGCG 100
CTTTTTCAGT GGGGCAGGGC AGGAAGCAGG CGGGACCAGG CAGCCAGTTC 150
25 TCAAAGGCTG CGGGGCCAAC TAGAGGCCAC AGCCCCTCAC CCCTAGACAC 200
TGCCAACCAG AACTGACACG CGACCTCCTG GCGCTGACG CCATTAAAC 250
CAACGTTGGC GCCCGGCG 268

30

(2) INFORMATION FOR SEQ ID :682:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :682:

347

GCCACCGCCG AGGAAAACCG TGCACTGTTA GCCATGATCA ACCCCACCGT 50
GCTCTTCGAC ATTGACATCG ACGGCTGAGC CCTTGACCTA GTCTCCTTTG 100
5 AGCTGTTTGC AGACAAGGTC CCAAAGACAG CAGAAAATTT TCGTGCTCTA 150
AGCACTGGAG AGAAAGGATT TGGTTATAAG GGTTCCTGCT TTCACAGAAT 200
TATTCCAGGG TTTATGCGCC AGGGTGGTGA CTTACACAGC CATAATGGCA 250
10 CTGGTGCGAA GTCCATCCAT GGGGAGAAAT TTGAAGACGA GAACTTCATC 300
CTAAAGCATA CGGGCCCTGG CATCTTGCCC ATGGCAAATG CTGATCCTGA 350
15 TACA 354

(2) INFORMATION FOR SEQ ID :683:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :683:

CCTCTCCGTG AGGACAGGGC AGTCTTGGTG CGCAGCCCCT CTCCTCTCTG 50
30 TCCCCTGACA CTCCACAGTG CGCCTGCAAC CCAGGCGGCC TTATCCGCGC 100
AGTGGCGGCA GTTCAGAAAT AAAGGGCCCA TTTGCGGGAT GCCGCATT 148

35 (2) INFORMATION FOR SEQ ID :684:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

348

(xi) SEQUENCE DESCRIPTION: SEQ ID :684:

	AGCACCGAGG CGCTCAAGGT CCTGGGGAAC CCCAAGAGCG ACGAGACGAA	50
5	CGCGAAGGCG CTGGACTTTG AGCACTTTCT GCCCATGCTG CAGACAGTGG	100
	CCAAGAACAA GGACCAGGGC ACCTATGAGG ATTATGCCGA AGGACTTCGG	150
10	GCGCTTGACA AGGAAGGAAA TGGCACCGTC ATGGGCGCTG AAACCCGGCA	200
	TGCTCTTGCC AACTGGGCG AGAAGACGAC AGAGGAAGAA GCAGAGACGC	250
	TGGCGGCAGG GCATGAGGAC AGCAATGGTT GCATCAACTA CGAAGCATTT	300
15	GTGAGGC	307

(2) INFORMATION FOR SEQ ID :685:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 174 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
25	

(xi) SEQUENCE DESCRIPTION: SEQ ID :685:

30	CCATCTCAAG GCGATCCATG GAAAGCTTCC TGGGGAACGT ATGCTAGCAG	50
	AGCTTCTCCC CGTGAATCAC ATGCCGGAGA TCCCACTCTT AGCTGGCAAA	100
	TGAATCCGAA TTGACACAGC AGCCCCATAA GCATCAGCCC TGTAGAGTGA	150
35	GGAGCCATCT CTAGCGGGCC CTTC	174

(2) INFORMATION FOR SEQ ID :686:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 106 base pairs
	(B) TYPE: nucleic acid

349

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :686:

ACATGCCAAA GAAAGCGTGC ATATTAGCCT ATAGAACCAC AGTAATCACA 50

10 CTAGAGAAAT TCCACTGCTA CAATAAATG TAATCGGAAG CATCTTTACT 100

TATAAA 106

15

(2) INFORMATION FOR SEQ ID :687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

20

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :687:

CAGATTTTTT TCAATTCTCC ACCCGCCAAA AGGGGAAGGG CTTTCCCCCA 50

GAGAAAAGGA AAGGGGGGAA AAGGGGAAAA AACCCAACCC AAAACCA 97

30

(2) INFORMATION FOR SEQ ID :688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :688:

350

GCCTCTCTCT GGGCAAGTTC ATGGCTTCTG TGAGCCCTTT NACTGACCTC 50
CAGACACTGT TAGGCTGGAG CCTCGGTAGC CGTTCCTCCT GCCCACTGGA 100
5 CCTTCCAACA GGCCCTCCTC CCCTCCTTGA ACCGGCCCTT CCTGGCCTTT 150
GAATAGAGTC TAAGCGAACG AC 172

(2) INFORMATION FOR SEQ ID :689:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :689:

20

GCCACCGCCG AGCTCACCCC TCGGGTGCAC GCCTTCCTTG GACAAGTTTT 50
TGGCTTCTGC GAGCCTTTTA CTGACCTCCA AACGCTGTTA AGCCGGAGCC 100
25 TCGGTAGCCG TTCCTCCTGC CCACTGGACN TCCCAACGGG CCCTCCTCCC 150
CTCCTTGAAC CAGCCCTTCC TGGCCTTTGA ATAAAGTTTA AGCGAGTAGC 200

(2) INFORMATION FOR SEQ ID :690:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :690:

40

GCCACCGCCG AGCAGCAGCT TACAGCCAGG GCAGCTTTGA ATGCGGCCCA 50

351

ACACAAATTC ACAAGTGNTC TCAAAAAACT C

81

(2) INFORMATION FOR SEQ ID :691:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :691:

15 TTCCTAACCG ATCGAATGAA GGATTCAAAA TTAACCACTC CAAGGGGGGA 50
TTGAAGGAAG AACCACTCTT AACGGACAAA AAGAAAGAAA GGGGAGGGAG 100
TAACAGGGAT ATGAGCTCTA GCCGCCCAAG CTAGCAATGG CAACCCTTCT 150
20 GGGTCCCCTT TCAGCATGCG GAAGCTTTTC TTCGACTTCA CTCCATAAAC 200
AGCTGACGCT CAAAAAG 217

25 (2) INFORMATION FOR SEQ ID :692:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :692:

CGGCCTTCTG GAAACCCATG AAAAAAAAAA GTTCGCACCC TCCAAGGGGA 50
GAAGAGTAAG AGACAGCTTT CA 72

40

(2) INFORMATION FOR SEQ ID :693:

352

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :693:

10

TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGC AGGGGAAGCA 50

GAAAAAGGCA AACAGAAGA AGGAGGAACC CAAGCAGCTT TCGGGCTTCG 100

15

CGTCCAACCC TCTTGCCCTT CACCTACGCG CCTAGAGCCA GTCCCACCAC 150

GCTCGCGTTT CCTCCTGTAG CGCTCACAGG CCCAGCACC GATGGCATTG 200

CCTTTGACCT AAGCCTACAG CAGGGCCCTT TTGTGCTTCC TTCCCCTCAG 250

20

GCAGCCTCTT TCCCCCTGGG CCACTCCCGG GGGTGAGGGG GTTGTCTTC 300

CCGATGCTTT TTGTTACCGT GGGGTTTGC 329

25

(2) INFORMATION FOR SEQ ID :694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :694:

TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGG CCTGCGCCGA 50

ACAAATGTAC GGAATGCGTG AGTCCCTCTG GGAGGCCG CACGGATCCG 100

40

GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG CTGCGGACCA 150

353

GGATGCAGTG TCAGGCATGG GAGTCATTGC CCACATCATC GAGAAGGACA 200
 AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC CTGTTCCCAG 250
 5 AGCCCACTTT TTTTTTTTTT TTGGAAATAA AATAGCCTAT CTTTCG 296

(2) INFORMATION FOR SEQ ID :695:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :695:

GCCAGCACCG ACCTAGCCTA AGCCGTCTAG AACCACCTAA GCCCCTAAGG 50
 20 AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGC GCAGAGG 100
 CGTGTCTTAG CACTAACCTC CTCCCTAGCC CTTATTGG TGGCAGAAGT 150
 25 GGCCTCCACC CCTTCACCGT TAAAAATAC TCCGTGGAGA AAAGAAAGCT 200
 TNAAGGAGTA G 211

(2) INFORMATION FOR SEQ ID :696:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :696:

40

GCCTGCACCG ACAATGCCCA GAACTCCAGA ACTTCACCTA TCACGTATCC 50

354

CCAACAACAC AGACGGCGAA AACAAAACAA ACTTAAACCT AG

92

(2) INFORMATION FOR SEQ ID :697:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :697:

15 GCCAGCACCG AGGCCTAGGG TAGAGCAGAC TGTGGCTTTA CCTCGGTGTC 50
CTACCAGCAA GGGGTCCTAT CTACCACCAT CCTCTATGAG ATCCTGCTAG 100
GGAAGGCCAC CCTGCATGCT GCGTTGGTCA GCACCCTTGC GCTGATGGCC 150
20 ATAGTCAAGA GAAAGGATTT CTGAAGGCAG CCCTAGAAGC GGAGTTAGGA 200
GCTTCTAACC CGTCATGGTT TAAATACACA CCCTTTTTTG GACAGCGCTT 250
CTGAAGAGCT GCTCTTACCT CTCTGCATCC CAATAGATAT CCCCCTATGC 300
GCATGCGTAC CTGT 314

(2) INFORMATION FOR SEQ ID :698:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :698:

40

GCCACCGCCG AGTTCACCCC TGCAGTGCAC GCCTCCCTGG ACAAGTTCCT 50

355

GGCTTCTGTG AGCACCGTGC TGACCTCCAA ACACCGTTAA GCTGGAGCCT 100
CGGTAGCCGT TCCTCCTGCC CACTGGACTC CCAACAGGCC CTCCTCCCCCT 150
5 CCTGCACCG GCCCTTCCTG GTCTTTGAAT AAAGTCTAAG CGGGCAGC 198

(2) INFORMATION FOR SEQ ID :699:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :699:

GCCAGCACCG ACAGCAACAA AAATGTTCCC ACAGAGATCA GGATGACTTG 50
20 CTGAAGCTCA GTGGAGGCTA AAAAGAGGAC ACAAAGTGA ACAGAATGAC 100
CTTCCTACGC ACAACACAAA CACCACTTAA TGCTCCATCC ACGCTGCTTA 150
25 AAGAGCATTC CTGTCCTAGC AAAATGGGCA AGTCCCTCTA CCCCCACCC 200
TTAGCCGGCA TGCTTACATT AATAGCTAGA 230

(2) INFORMATION FOR SEQ ID :700:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :700:

40

AGCAACAAAA ATGTTTCCAC GGAGATCAGG ATGACTTGCT GAAGCTCAGT 50

356

GGAGGCTCAA AAGAGGACAC AAAAGTGAAC AGAATGATCT TCCTACGCAC 100
AACACAAACA TCAGTTAATG CTCCATCCAC GCTGCTTAAA GAGCATTCCT 150
5 GTCCTAGCAA AATGGGCAAG TCCCTCTACC CCCACCCTC ACTTGGCATG 200
CTTACATTAA TAGCTAAAGT CAATCCTGTA ATGAAATAAA GCAAATGGCA 250
GCTGTCTAGT AGCCTCCACT ACCGCAAATA TC 282

10

(2) INFORMATION FOR SEQ ID :701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :701:

GCCTGCGCCG AACAAACGCA CGGAATGAGC GAGTCCCTCT GGGAGCCCAA 50
25 CATGGATCCG AATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100
CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150
GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCCGAA TGGACTAACC 200
30 CTGTTCCCAG AGCCCACTTT TCCCCTATTT TGGAAATAAA ATAGCCTGTC 250
TTTCG 255

35

(2) INFORMATION FOR SEQ ID :702:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

357

(xi) SEQUENCE DESCRIPTION: SEQ ID :702:

5 GCCTGCGCCG AGCACAAGAC AATGATGAAC ATTCTAAAAA AAAAGAATGA 50
CGCACATTTT AATAAAGCAC AGCACAAACT GTTCTTTCC 89

(2) INFORMATION FOR SEQ ID :703:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :703:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGCCGC ACCCCCGCTA 50
GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GTCGGG 96

(2) INFORMATION FOR SEQ ID :704:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID :704:

35 GCCTGCGCCG AACAAACATA CAGAACGCAA CGAGTCCCTC TGAAGGCCCA 50
ACACGGATCC GAATCACCTG GCCCGAAACC ACCTACCTAG CCATGATGAA 100
40 TGCTGAGGAC CCAGATGCAG TAC 123

(2) INFORMATION FOR SEQ ID :705:

358

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :705:

10 GCTTGATGCC TGCGCCGAAC AAACATACAG AATGCGGCGA GTCCCTCTGG 50
ACGCCCAACA CGGATCCGGA TCACCTATCT GAAACCATCT CCCAAGCCAT 100
15 GCTGAATGCT GCGGACCAGG ATGCAGTGCC AGGCATGGGA GCCATTGCCC 150
ACATCACCGA GAAGGACAAA ATCACCACCA GGACACTGAA GGCCCGAATG 200
GACTAACCTT GTTCCCAGAG CCCACTTTTT TTCTTTTTC AATAAAAC 250
20 AGCCTGTCTT TC 262

(2) INFORMATION FOR SEQ ID :706:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :706:

35 GCCAGCACCG ACCTAGCCTA AGCCGTCTAA AACCACCTGA GCCCCTGAGG 50
AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG 100
CGTGTCTTAG CACTGCCCCC CTCCCTAGCC CTTATTTGG CGGCGGAAGC 150
40 GGCCTCCACC CCTTCCCTGT TTGCAAACAC TCTGCGGAGA AAAGAGGACT 200

359

TCAGGGAGT

209

(2) INFORMATION FOR SEQ ID :707:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :707:

15 GCCAGCACCG AGATGACGAG CTTTCTGCTG CCACCCACAA GCAGAGGGAC 50
TCGGAGATCA CGCAGCAGAA GCAGAAAAAG GCAAACAAGA AGAAGGAGGA 100
ACCCAAGCAG CTTTGCGGCT TCACGCCCAA CCCTCTCGCC CTTACCTGT 150
20 GAGCCTGGAG CCAGTCCCAC 170

(2) INFORMATION FOR SEQ ID :708:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :708:

35 GCCACCGTCG AGGATTCAGC AGCCTCCCCC TTGAGCCCCC TCACTTCCCG 50
ACGTTCCGTT TCCCCCTGCC CGCCTTTTTC CGCCACCACC GCCGCCGCCT 100
TCTGCAGGCC GTTTCACCG AGGAAAAGGA ATCGTATTGT ATACCCGCTA 150
40 CCCAGAACCT 160

360

(2) INFORMATION FOR SEQ ID :709:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :709:

GCCAGCACCG AGCAACCTGG GTCCAAATAA AACTAAACT GCAAACCTCT 50

15

G 51

(2) INFORMATION FOR SEQ ID :710:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :710:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

30

CAGGATTCTC TTCT 64

(2) INFORMATION FOR SEQ ID :711:

35

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

361

(xi) SEQUENCE DESCRIPTION: SEQ ID :711:

CCAGCCAAAG ATTCCCAGGC TTTCTTGTCT CAGCAACTTT CCCATCTTCT 50
5 CTCTCTTGGA TGATGTTTGC CGTCAGCATT CACCAAATAA ACTTGCTCTC 100
TGGG 104

(2) INFORMATION FOR SEQ ID :712:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :712:

20

CTAGAAATAG ACCCACAATT TAGAGACAAT CTATACTAGA TTTATCTCCT 50
TTGTTTTTAG TTGAAGGC 68

25

(2) INFORMATION FOR SEQ ID :713:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :713:

AGCGAATGTA AGGGGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT 50
GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT 100
40 GTGCTTGGGT CGCTGTCTAC TGCTCCT 127

362

(2) INFORMATION FOR SEQ ID :714:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :714:

CTTGGGAGAT AACAGTTTCC CCTCTCCCTC CCCCTGCAGA TTTCCAGCGC 50
15 CCGGACCAAG GCCAAGTAAG CCTCTACAAA CCTAGCATTT 90

(2) INFORMATION FOR SEQ ID :715:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :715:

CCAGCGCCGA GGTGTATAT TTGTAGGTGC AGGCACACGA CCAGGACACA 50
30 ACAAAAATCT GAAACATC 69

(2) INFORMATION FOR SEQ ID :716:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

363

(xi) SEQUENCE DESCRIPTION: SEQ ID :716:

GCCGAGGAGA ACCCCCGCTC CCTGAGGAGG ACCTGTCCAA ACTCTTCAAA 50
5 CCACCACAGC CGCCTGCCAG GATGGACTCG CTGCTCATTG CAGGCCAGAT 100
AA 102

(2) INFORMATION FOR SEQ ID :717:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :717:

20

AGCGAATGTA ACCCGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT 50
GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT 100
25 GTGCTTGGGA TACGCTGTCT ACAG 124

(2) INFORMATION FOR SEQ ID :718:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :718:

GGAAAACCGT GTACTATTAG CCATGGTCAA CCCCACCGTG TTCTTCGACA 50
40 TTGCCGTCGA CGGGAGCCCT TGGCGCGCGT CTCCTTTGAG CTGTTTGCAG 100

364

ACAAGGTCCC AAAGACAGCA GAA

123

(2) INFORMATION FOR SEQ ID :719:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :719:

15 ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC 50

TTCT 54

(2) INFORMATION FOR SEQ ID :720:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :720:

30

GACCACAGGG CCTTCAATCC TTTTGTGTTT TCAACAGTCT TGCTGAATTA 50

AGCAGAAAGG GCCTTGAATC CTGGCCTGGA ATTTGGGCAG ATATAGCATT 100

35 AATAAACTG TGCACTC 117

(2) INFORMATION FOR SEQ ID :721:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

365

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :721:

GACCACCCCT TCCTTTTCTT CATCCAGCAC AGCAAGACCA ACGGGATTCT 50

CTTCT 55

10

(2) INFORMATION FOR SEQ ID :722:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :722:

GACTTCACGA ACTACACAGG TCTTACCATT GACCTAAGAT CAATCTGAAC 50

25 ATTCTTAGCC CAGTCAGGGA GCTCTGCTTC CTAGAAAGGC AT 92

(2) INFORMATION FOR SEQ ID :723:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :723:

TATTTCTAGG TGCAGGTATA TGATTGCCAT ATAATAAAAA TCTGAAAACA 50

40

TCCCC 55

366

(2) INFORMATION FOR SEQ ID :724:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :724:

GTGTACTATT AGCCATGGTC AACCCACCG TGTCTTCGA CATTGCCGTC 50

15

GACGGGCGAG CCCTTGGCGC GCGTCCTTG AGCTGTTGC AGACAAGGTC 100

CCAAAGACAG CAGAAAAATT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA 150

TTTGTTATA AGGG 164

20

(2) INFORMATION FOR SEQ ID :725:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :725:

GTGAGAAGCT GCAGCGGTGA CCTGGAGGCT GCGATGTGGA GGTGGAGGAC 50

35

ACACCCTCAA CCGTTGCTCC TGTAGCTTCC GAGTCCTGGT GGTGTCGGCC 100

AAGTTCAGTA 110

40

(2) INFORMATION FOR SEQ ID :726:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 base pairs

367

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :726:

CCGTGTACTA TTAGCCATGG TCAACCCAC CGTGTCTTC GACATTGCCG 50
10 TCGACGGGAG CCCTTGGCGC GCGTCTCCTT TGAGCTGTTT GCAGACAAGG 100
TCCCAAAGAC AGCAGAAAAT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA 150
15 TTTGGTTATA AGG 163

(2) INFORMATION FOR SEQ ID :727:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :727:

GAGGGCGAGT TCGAGGAGGA GGCTGAGGAG GAGGTGGCCT AGAGCCTTCA 50
30 GTCAGTGGGG AAAGCAGGGA AGCAGTGTGA ACTCTTTATT CACTCCCAGC 100
CTGTT 105

35

(2) INFORMATION FOR SEQ ID :728:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

368

(xi) SEQUENCE DESCRIPTION: SEQ ID :728:

5 GCCAGCGCCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG 50
ACCTAAGATC AATCTAAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT 100
AGGAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTCGA GGCCGCCACT 150
10 GGAAGACGAA AAATAGAACT CCCTTAGAGT AGACAA... 186

(2) INFORMATION FOR SEQ ID :729:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :729:

25 GCCAGCGCCG AGGTTGCATA TTCTAGGCGC AGGTATATGA TTGCCATATA 50
ATAAAAACCT GAAAACATCC CACCCGGGAA AAAAAAAAAA AAAAAAAAAA 100
AAAAACACCC CCCCCCACA AAAA ACTCAA ATTCCCTCC CAAAAAACCC 150
30 CCTCAAATC AAAAAAC 167

(2) INFORMATION FOR SEQ ID :730:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :730:

369

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

CAGGATTCTC TTCT 64

5 (2) INFORMATION FOR SEQ ID :731:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :731:

GCCAGCGCCG AGACCCTGGC GGCCTACCGG CCCCCCGTGC ACCCCCGCTA 50

20 GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

(2) INFORMATION FOR SEQ ID :732:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :732:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

35 CAGGATTCTC TTCTGCAGCC GCCACCGCGT CGGA 84

(2) INFORMATION FOR SEQ ID :733:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

370

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :733:

GCCAGCGCCG AGATCCTGGC GGCCTACCGG CCCTCAGTGC ACCCCCGCTA 50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

10

(2) INFORMATION FOR SEQ ID :734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :734:

GCCAGCGCCG AGATCCTGGC GGCCTACCAG CCCTCCGTGC ACCCCCGCTA 50

25 GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

(2) INFORMATION FOR SEQ ID :735:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :735:

GCCAGCGCCG AGATCCTGGC GGCCTACCAG CTCCTCAGTG CACCCCACT 50

40

AGCACCCAC CCCGCATCTA TCGCCCAATA AAGGCATCTT TGCCGGG 97

371

(2) INFORMATION FOR SEQ ID :736:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :736:

GCCAGCGCCG ACCACAGGGC CTTGAATCCT TTTTGTTTT CAACAGTCTT 50
15 GCTGAATTAA GCAGAAAGGG CCTTGAATCC TGGCCTAGAA TTTGGGCAGA 100
TACAGCATT ACAAACCGC GCATCTC 127

(2) INFORMATION FOR SEQ ID :737:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :737:

30

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50
CAGGATTCTC TTCT 64

35

(2) INFORMATION FOR SEQ ID :738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

372

(xi) SEQUENCE DESCRIPTION: SEQ ID :738:

5 GCCAGCGCCG ACAATGCCCA GAATCCAGAA CTTGCCTAT CACTCTCCCC 50
AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :739:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :739:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGTGCA CCCCCGCTAG 50
CGCCCCACCC CGCGTCTACC GCCCAATAAA GGCATCTTTG CCGGG 95

(2) INFORMATION FOR SEQ ID :740:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :740:

35

GCCACCCCGA AGACGTATCA AGGCCCTCGA ACAACCCCGA GAGCTGATGA 50
GATGAATGAG AAGATGCCGA ACTTTGCGCA CTCCATGCCC CTGCTGCAGA 100
40 CAGTAACCAA GAGCAAGGAC CAGGGCACCC ATGAGGATTA TGTCCAAGGA 150
CTTCGGGTGT TTGACAAGGA AGGAAATGGC ACCGTCATGG GTGCTGAAAT 200

373

CCGGCATGTT CTTGTCACAC TGGGTGAGAA GATGACAGAG GAAGA

245

(2) INFORMATION FOR SEQ ID :741:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :741:

15 GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTCGTCTAT CACTCTCCCC 50

AACAACTAG ATGTGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :742:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :742:

30

GCCGGAGCCA AAGCAAGCCA GAAGACTAAC AGTACTAACT ACAAATATTC 50

GCACCTCGAT CGCAGTACCC AGGTTCTCAC GTAGCTGAAG NAATGTATTA 100

35 CTCTGATAGT CTTCATTCGG ATAGACTAAA GCGTGTGCTG ACTGGAGATG 150

AGGTAAAGAA GATATGTATG CAACGTCCAG TCAAAACGGA TGGCAAGGTT 200

CGAGTCATGT CATATACCTT GCTGGATTAA TGGATGTCAT TA 242

40

(2) INFORMATION FOR SEQ ID :743:

374

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :743:

10

GCCTGCGCCG ACCACCCCTT CCTTTTCTTG ATCTAGCACA GCAAGACCAA

50

CGGGATTCTC TTCT

64

15

(2) INFORMATION FOR SEQ ID :744:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :744:

GCCAGCGCCG AGGTTGTATA TTTCTAGGTG CAGGTATATG ATTGCCATAT

50

AATAAAAATT TGAAAACAT

69

30

(2) INFORMATION FOR SEQ ID :745:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :745:

375

GCCAGCTCCG AGGTTGTATA TTTCCAGGTG CAGATATATG ATTGCCATAT 50
AATAAAAATC TGAAAACATC CCAC 74

5 (2) INFORMATION FOR SEQ ID :746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :746:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTGTCTAT CACTCTCCCC 50
AACAACCTAG ATGTGAAAAC AGGATAAACT TCACCCAG 88

20

(2) INFORMATION FOR SEQ ID :747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :747:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTGTCTAT CACTCTCCCC 50
AACAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG 88

35

(2) INFORMATION FOR SEQ ID :748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double

376

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :748:

GCCAGCACCG ATGAATTCCC TTTGACCCAA GTCTGCAGCA GGTCCCTTTT 50
GCGCTTCCTT CCCCTCAGGC AGCCTCTTTC CCCCTGGGCC ACTCCCGGGG 100
10 GCGAGGGGGC TACCCCTTTC CCAGGCTTTT TATTCCCGTG GGGCTCACCC 150
CAAAGCATTAA AAAGCAGCTT TGCAATTC 178

15 (2) INFORMATION FOR SEQ ID :749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :749:

GCCAGCACCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG 50
ACCTAAGATC AATCTGAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT 100
30 AGAAAGGCAT CTTTCGCCAG TGGATTCGCC CCAAGGTTGA GGCCGCCATT 150
GGAAGACGAA AAATTGCACT CCCTTGGCGC AGACAAACAC CAGTTCCCAT 200
35 TGGCGCTGCT GCCTATAACA AACACTTTTT TTTT 235

(2) INFORMATION FOR SEQ ID :750:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: doubl

377

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :750:

GCCTACGCCG AAAACCCCTT CCTTTTTTTC ATCCAGAAAA GCAAGAGAAA 50

AAGGATTCTC TTCTGCGGCC GCCAACGCGT CGGAGAT 87

10

(2) INFORMATION FOR SEQ ID :751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :751:

GCCTCCGCCG ATTCGTGACC AAGAAGGCTC TATGCATTCA GGCTTTCAG 50

25 GAGACTCAAA AGCTGAAGAA GCAAAGAAGA GCCTTAAAGG CTGCAGCAGC 100

AGTCCNAAAA ACAAGCAGAG CAGAGGAACC CAGACAGCCC TGCCAAAGCC 150

ATGCCAAAGA CACTCAAAGA 170

30

(2) INFORMATION FOR SEQ ID :752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :752:

378

GCCAGCACCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT 50
AATAAAAAAA TGAAAACACC CC 72

5 (2) INFORMATION FOR SEQ ID :753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :753:

GCCAGCGCCG AGGACACCAA GAAGGTTTGG GACAGCGTGG GCATCGAGGC 50
GGACAACAAC CAGCTCAACA AGGCCATTAG TGAGCTGAAT GAAAAAACA 100
20 TTGAAGACGT TATTGNCCAG GA 122

(2) INFORMATION FOR SEQ ID :754:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :754:

35 GCCACGCGCC ACTGAACTG CACCGACCCC CCCTCGAGGA CCTGCTCTTA 50
GGTTCAGAAG CAAACCTCAC GTGCACACTG ACCGACCTAA GAGACGCCTC 100
AGGCGCCACC TTCACCTGGA CACCCTCAAG CGGGAAGAGC ACTGTTCAAG 150
40 GACCACCTAA GCATGACCTC TACGGCTGCT ACAGCGTGTC CAGTGCCCTG 200

379

CCGGGCTGCG CCGAGCCATG GAACCATGGG AAGACCTTCA CTT

243

(2) INFORMATION FOR SEQ ID :755:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :755:

15

GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT

50

AACAAAAACC TGAAGCATC A

71

(2) INFORMATION FOR SEQ ID :756:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :756:

30

GCCACCGCCG AGTGACGCCA AAGCCCTTGG TTGACTCTAA CAGCCCCGTG

50

GGCGCGCGGG AGGCCGGGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT

100

35

TAGTGCTTTT TCAGTGGGGC GGGGCGGGAA GCAGGCGGGA CCAGGCAGCC

150

AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA

200

GACGTCGCCA ACCAGAACTG ACGCGCGACC TCCTGGGCGC TGA

243

40

(2) INFORMATION FOR SEQ ID :757:

380

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :757:

10

GCCTGCGCCG ACCACCCCTT CCTTTTTTTT ATCCAGCACA GCAAGACCAA

50

CAGGATTCTC TTCC

64

15

(2) INFORMATION FOR SEQ ID :758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :758:

GCCAGCACCA AGTGACGCCA AAGCCCCTAG TTGACTCTAA CAGCCCCGTG

50

GGCGCGCGGG AGGCCGAGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT

100

30

TAGCGCTTTT TCAATGGGGC AGGGCAGGAA GCAGGCGGGA CCAGGCAGCC

150

AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA

200

35

GACGTCGACA ACCAGAACTG ACGTGCAGCC TCCCGGGCGC CGA

243

(2) INFORMATION FOR SEQ ID :759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

381

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :759:

GCCACACCAG ACTTTCGACC CCCCAACCCT CTGAGGAAGA TGGGGGCAAG 50
AAGATCACGC TCCCCGCCTG TTCCCCCGCC GCTTTTCTCC TCTCTTCTCT 100
10 CTTGCTCTC AGCTCCCCCT GTCCCTCAG CTCCAGACGT AGGGGAGGGG 150
TTGCCACAGA CTCCCTGCTT GAAGCCTGCC CTTGCCTAAG ATGCTGGTAA 200
15 TGGCCATGGT ACCCCCTTCC GGGCATCTAC TCTGGTTTTC GGCCA 245

(2) INFORMATION FOR SEQ ID :760:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :760:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT 50
30 AACAAAAACC NTGAAAAC 68

(2) INFORMATION FOR SEQ ID :761:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

382

(xi) SEQUENCE DESCRIPTION: SEQ ID :761:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50
5 AATAAAAACT GAAAACACCC C 71

(2) INFORMATION FOR SEQ ID :762:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :762:

GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC 50
20 AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :763:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :763:

35 GCCTGCGCCG ACAAACAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCCG 50
GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC 100
CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG 150
40 CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG 200

383

CGGATAGTCA CACTCCCTGC CGA

223

(2) INFORMATION FOR SEQ ID :764:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :764:

15 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50
AATAAAAATC TGAAAACACC 70

(2) INFORMATION FOR SEQ ID :765:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :765:

30

GCCAGCGCCG ACCGCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50
TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAAA CCAACCACC 100
35 TTTCTACGTA CCGTATAG 118

(2) INFORMATION FOR SEQ ID :766:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

384

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :766:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTGCCTAT CACTCTCCCC 50

AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

10

(2) INFORMATION FOR SEQ ID :767:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :767:

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTTGATCTTC AACTCTGCAT 50

25 ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTCAAT T 91

(2) INFORMATION FOR SEQ ID :768:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :768:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA 50

40

CATGGATCCG GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100

385

CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150

GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC 200

5 CTGCTCCCAG AGCCCACTTT TTT 223

(2) INFORMATION FOR SEQ ID :769:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :769:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC 37

20

(2) INFORMATION FOR SEQ ID :770:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :770:

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC 37

35

(2) INFORMATION FOR SEQ ID :771:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

386

(xi) SEQUENCE DESCRIPTION: SEQ ID :771:

5 GCCACCGCCG ACTCCAGGCA CTCACTCAA CTGATCTTC AACTCTGCAT 50
ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T 91

(2) INFORMATION FOR SEQ ID :772:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :772:

20 GCCTGCGCCG ANGCAATCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTTT 50
GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG 100
GTGAGGGGGT TACCCCTTCC CAGTGTTTTT TATTCCCGTG GGGCTCACCC 150
25 CAAAGTATTA AAAGCAACTT TGCAATT 177

(2) INFORMATION FOR SEQ ID :773:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :773:

40

AACATAAGAG GAGAAAGGAA GGGACATGAG GCATACCATT CCCCCCCCCA 50

387

GAATTAGAGG TAAAGGAATC CTAAAATAAA GAGCACAGCA GCAATCACAC 100

TCACAGGGTC CAGAGGCGTA TTCCTGGCCA TCTTCCTAGT ACTCGGTCCG 150

5 T 151

(2) INFORMATION FOR SEQ ID :774:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :774:

ATCTTAATGA ACATGGCATT TAAAATCCTG TAATTTCAA CAGTGAACCA 50

20

CAATGCCGTA TGATCTAAAG GCTGCTGAAC CACAGCGTGG ATACACTTAA 100

CTGAGCTCCT CGCTGGGTCA AAGCACTCAT CTCCGAGTCT AAAGCTACAC 150

25

ACTATGGAGC ACACAACTCT GCCTCGCGCT GACACCAGAC AAACACGGCG 200

GGAGCTGAGG CGGACAGCTA CAGGACCACG AGCATAGACC ACGGCACCTG 250

AGACCATCTC TACGCAAGGA CTTAAGGAAG CAAATATAAT ATTAAAATA 299

30

(2) INFORMATION FOR SEQ ID :775:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :775:

388

TGAAGGAAAT GACTACCTTG CACTACATGA AAAGGATATC GTTGCCATTG 50
TGGCGTAATT TTCGTGCCGA GTGAATGTGG CGCAAACAAC TATATATCNA 100
5 AACCGTATAT TTAAATGAA TTACTAGAGA GGAATGTAA TCATGGCAAA 150
AGAAATTAAG TTTTAAGAAG ATGCTAGTGC TAAGC 185

(2) INFORMATION FOR SEQ ID :776:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :776:

20

ATCCAAGCCC ATACCCATCA ACAATGGGAC AGCGATTGGA TCACCAGCCA 50
TTTCACCACA CATGGCAACA AACTTACCTT CTTTAAGAGC GGCAGTAATC 100
25 ACATCGTCGA TCAAACGCAA AATCGATGGG TTATAAGGTC GATACAAATA 150
AGCAACCTTA TCATTACCAC GATCTGCAGC CATCGTATAA CCAATCAAAT 200
CGTCGGTACC AATCGAGAAG AAGTCCAATC CCTTAGCAAA CTCATCAGCC 250
30 AACAT 255

(2) INFORMATION FOR SEQ ID :777:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

389

(xi) SEQUENCE DESCRIPTION: SEQ ID :777:

	AGATTCTGCA GTGTAATATG ACCAAATCAA ATCCGTTGTA TGATCGAATA	50
5	AGGCCGTCAT AAAGTAAGTT GAAAATTTTCG TTCTTGGCTG AATCGTGTTA	100
	AACCGTTGTA CACAACGTAG TAAAATTCAT AACCCATCTG CATACCAATC	150
	GTCAGCCGTG ATGCATTTAC TCACTTTACG TCGATGAATG TCAAACATCG	200
10	CACCTTTTCA ATGTTTACTA AAAACATAGC ACGCAATAT	239

(2) INFORMATION FOR SEQ ID :778:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 252 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :778:

25	ACTGAACAAC GTAAGGTCTT GACTGACACT TACAAGTTGG ATGAATCTGA	50
	AATAAAGTTG GTATTGTTTG AAGCAGCCCA ACAATTTTCGA ACATGCTACA	100
	AGACCGTCGT TTGACTGACA AGGCCTTGAA GTACATGACT GACAACAACG	150
30	TCGATCTTCG CCTAGGCGCC ATGGTCACTG GTGTTGACGA AAATGGCGTG	200
	ATTTTAAAGG ATGACTCAAC TTCGCCAACT CGGTTCTCTA TTAGGACAAC	250
35	TA	252

(2) INFORMATION FOR SEQ ID :779:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 265 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

390

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :779:

TCGGATTTAT ACGGCTGTTA GTGCTATCGG CGTCTGGTAT GTGTTATATA 50
TCGCCTATCG TTTTGGGCC AATGGGCGTT GGCTACGCGG GGCAATGATT 100
10 GCCATCGTTT TTGTTATCTT GACTTATTTT GTCATTTTAA ATATTATTTA 150
ACTATTTTAC AAATAAAGTG GTCAAATGGG ATATTTTGCC AAAAATAGAG 200
15 AAAGTGTTAG GCGGCCACACA GCTGGAGGAA GAGAAAGCGG CTGTGCATGA 250
AGTTATTGCA CCCGC 265

(2) INFORMATION FOR SEQ ID :780:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :780:

30

CTCAGCTGGA CCAAATTAGT TGAATTACTC ACCATCAATA AACTATAAAT 50
GGCGCCAATG ACCAACCCGC CAACGATTCC CGTTGTCAAA GAACCTAATA 100
35 ACAAGTAACC AACCGCAGCC CCAACAAGCC CAACTAGGTT TAAAAAACC 150
AAGCAAAAGG CCAACTGTCC GTCGTTTATT GGATTGTATC TGCTCATATA 200
ACATTAAAC TTAACCGTTG GCACTTCTTT CTCAGACCCG CCGATACTG 249

40

(2) INFORMATION FOR SEQ ID :781:

391

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :781:

10

GAGAGAACCC ACCATAGTAC TGTCTCCTGC AGACAAGACC AACGGCAAGG 50

CCGCCTGGGG TAAGGTCGGC GCGCACCTGG CGAGTATGGT GCGGAGGCCC 100

15

TGGAGAGGAT GTTCCTGTCC TTCCCCACCA CCANNNACTA CTTCCCGCAC 150

TTCGACCTGA GCCACGGCTC TGCCCAGGTT AAGGGCCA 188

(2) INFORMATION FOR SEQ ID :782:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :782:

30

AATATTTATT TCATTGTTT ACTACCACTT CATTTTATTT GTTGCTGCT 50

GCCGTTTTAT TTATTTTAC TGAAAGTGAG AGGGAACCTT TGTGGCCTCC 100

35

AACCTTTTTC TGTAGGCCGC CTTAAGCTTT CTAAATTGG AACATCTAAC 150

AAGCTGAAGN GGAAAAGGGG GTTCGCAAA AT 182

(2) INFORMATION FOR SEQ ID :783:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs

392

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :783:

CACAGCCAGA GCTTCGTCCT CAGTGACCAC AGGGCTGAGC CAGGCTCAAC 50
10 CGGCTTCTGG CTCTTGTTTT GCAGAAGAAG AACTAGAAGC AAGGNGCTTT 100
CCTCCGGGTC CCAGAGCTGT TAGTGATGGA GCCAGGCCTG GGATCCAGCT 150
15 TTCCTGAGTT CCTGACCCCT GCTATTTTAT TAGTCAGCTC TCAGCACTTA 200
CCAGAGGAAC AGGCAGCCTT TTGGCTACTG CCTTCAGAGA AAGAGAGATG 250
AGAGAATTCA AATGCGTGTT GGTGTCCTG TTAGTACAAG CAGCA 295

20

(2) INFORMATION FOR SEQ ID :784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :784:

CAATAGCGAC TTCTGGTGTC AATTCGATAA TCGGCCAATG GATACTTCAC 50
35 GTGTGTTTCA TCGTCTGTAA TAACGGCGAA TGGTGTCACT TCAGAACCAG 100
TACCTGATGT TGTTGGAATG GCAACCATTG GTGTCAAACG CACTGGTAGA 150
ACTTCACGAT ACGCTTACGG ATGTCCATGA ACTTTTGTTT TATTTCCATG 200
40 AACAAATCCT TGATACCTTC TTCGTCTGAC AAAATACCTT CGTGACGTGT 250

393

TGAGTATTCG TACAAGAAGC GACCAATCTT ACCGGCATCA AGTGC

295

(2) INFORMATION FOR SEQ ID :785:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :785:

15 GTGTAAAGCG AGTAGCCCCC AAATCAGTCA TCTTGGCCTG AAGATGTAAA 50
CAAGGAGGTT TGCTTCCTGC AAGATGAGTA CTTACTGAG TTTGGTTTTTC 100
ATTTTTCCTA CACCGAAGCC ACCTCTGTCC ATCCAATGTT CATGTCTGTC 150
20 CGAGGCTGCG CAGGAGGTTA CGTCAAGATG TGGCCAATAA AGTCCAAAAA 200
GCGCTTTGAA TACTGTTCTG GGTTACGGT GGAGATCTCC GCGCAGCCAT 250
GTTTAACAGT TTTTGCAGCA TGGGCAGCTT TCTTTTTTGC ATCATAATGA 300
GTA 303

(2) INFORMATION FOR SEQ ID :786:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :786:

40

TATGGCGCGG ATCCTAACGG CTGGAATGAA GATATGCCAA CGTACAGCCT

50

394

CTATGACCCA GCCATGGGAT CAGGCTCATT GCTTTTGACG ACTGCTTCAT 100
ACATGAAGAA TGATGGTGTG CGTGGGGCCA TTAAGTACTA AGCCAAGAAG 150
5 TTATCACGAC AACCTATAAC TTGGGCCGAA TTAAGTTGAT GATGCACGGG 200
GTGGAGTATA ACGATATCAA TATCCATAAT GCAGATACCT TGAGTTCAGA 250
CTGGC 255

10

(2) INFORMATION FOR SEQ ID :787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :787:

CATTGAAAAG TGCCTGAAAA ATGGTAAATT CTTAAATGTG TGTGAGATTG 50
25 TCAGAATCAA CAAAAGTAGG TTGGTTAAAC ATATCTCTGG TACATCAAGG 100
GGCATGATAC AAACCACTCT AAAGACTGTT TATAAAGGAG AGAGCTGGCG 150
ACTTATTTTT ATTTTTTTTT TTTTGGACAG ACTCCCTTTG TCCCCAGGCC 200
30 GGAGTG 206

(2) INFORMATION FOR SEQ ID :788:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

395

(xi) SEQUENCE DESCRIPTION: SEQ ID :788:

ACAAATAGCG ACCTCCTGGA GAAAAATCGA AAACGGCCAA GTGGATACCT 50
5 CACGTGGTTC ACGTCTGAAC AACGGCGAAT GTGAGCTACC TCAGAACCAG 100
TACCCGAAGT TGCTGGAAGG CAACCACATT TGTTCAAAC GAGGCGTGGA 150
AGAACCTCAC GACACGCTTA CGGAGTCCAT GAACGCTTGT TGCAATCCAG 200
10 GAACAATTCC GCGACACCCT TCGTCTGACA AAAAACCTTC GTGACGCGTC 250
GAGTATCCGC 260

15 (2) INFORMATION FOR SEQ ID :789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :789:

AACCCACCAT GGTGCTGTCT CCTGCCGACA AGACCAACGT CAAGGCCGCC 50
TGGGGTAAGG TCGGCCTGCG CACTATGCGT GAGTATGATG CAGAGGCCCT 100
30 GGAGAGGATG TTCCTGTCCT TCCCCACCAC CAAGCCCTAC TTCCCGCACT 150
TCGACCTGAG CCACGGCTCT GCCGAGGTTA GGGGCCACGA CAAGAAGGTG 200
35 ATCGACGC 208

(2) INFORMATION FOR SEQ ID :790:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

396

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :790:

AAAAGAAGTA CGGTAAGGCA AATCCTGAAA TTAAGAGTTA CTATGTGCCT 50
GAAAATACAT TGTCTACTC ATTTAGTGTG ATGGCAATGG GCGCCGGCGC 100
10 ACTCTTGCTA TCGACCATCG TCGCGCTTTG GATGAACCGT CGTAAGTCAC 150
AATTAATGTA GACACAACGT CGATTCTCGT GACTTATGGG GATCGCAACT 200
15 TTCGCGCCAT TCTCGATCAA CACAGCCGGT TGGTCAGTGA CTGAATTAGG 250
TCGTTATCCA TGGGTTGTTT ATGGCTTGAT GCTAATAGC 289

20 (2) INFORMATION FOR SEQ ID :791:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :791:

TTTCCTGTGG AAGTAGTTAA ATTGATAAAT TCCAAAAATT TGGCAATTAA 50
TTGCTCATT TTAATGGTAG AGTTTCCATT AATGAAGTTG GAAAATACGG 100
35 TGAATCTTTC AATGAACTCA GTTAGACATT CGGAATGAGC TTCATACATT 150
GTCTTATTAT CTTTCTTCAA TTTATCCTCC AAATCTGGGA ATTCTGATAA 200
CCAAATTGAA GCACCTTATC TATGATCCGG GC 232

40

(2) INFORMATION FOR SEQ ID :792:

397

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :792:

10

TTTCAACAAA CAGAAACCAA TTTCCAACCA GAGGGCGATT TCTCCTTGTC 50

TGGTAATATC GAACAACTA TTTTAAAGAA CTGATTTCT GGCAACATTA 100

15

AGAGCGCTGT GAAAAATTCT CTAGAGAATG ACTTACTAAC GGAGGCCATG 150

GCGATCGCAT TAGATTCAA TAACGAAAGA TCAAAGGAAA GTGTCAAGAA 200

TGCCTATTTC GCGAAGTATG GATCTAAATA AC 232

20

(2) INFORMATION FOR SEQ ID :793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :793:

GGGAACATAT CTTACGGTA GTGANCCCAG TGACCAGATG TCTTATACAA 50

35

GTTCAAGTTA GACAAAACGG GTGTATACAC GTGTTGGTAA CCATTGGCCA 100

ATTCTTTGTC GGTGATGTAA CGTTCAACTT GACGGCGAAG CGATTGCCCC 150

ATTTGGTAAC CAACTGGCA AACCTGAACC CACTTCTTGA CTCGTAAAGA 200

40

ACAAGTCCAT GTCACGACCA ATCGTCCGGT GGTCACGTTT TTAGCTTCT 250

398

TCACGACGTG CAATTCTGCT TCAACGTCGG CTTGCTTCCA TT

292

(2) INFORMATION FOR SEQ ID :794:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :794:

15 CAGCAGGCAC AACACCATCG GTTGTCGCTG AAAGTATTTT TAAGTCTTTG 50
GCCAAGAAGT CAGTTTCAGC TAAGTTAGAC GGCACCTATG CGGGTATGCA 100
TGATGTCATT CCTGCATCCG ATGATTTTTTA ATTAATTACA ACAACTGATG 150
20 ATGAAGCGTC GAATTCGTCG CGTCATTCTG CCTCACACTC ACAGGCACAA 200
GCCTTAAAGC ATTTGCCAAA GTTTGCTAAC ATGCACTTTG GCGCGGCAAC 250
25 CATTATTGA AAATGGTTTC TACTATGATA CAAATAAC 288

(2) INFORMATION FOR SEQ ID :795:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :795:

40 GTGGCTATGT ATAAGCAGAT ATTATCTAGT AAATGTAAAG TGAACCCAAT 50
CGATAGACCC AAAAAGTGTT TTAAGTGGAA AACACCTTAT GAGGTTTATT 100

399

TTGATGAAGT GTTGCA GTTGTGATAAT TCAAGGCATT AAGGCAATAT 150
CTCAATCACC GCATTTTCCA CAACCGGCCA CAAAACAGCT CGTCTATTTT 200
5 GAGGTCACTT ACGGCGTCCA GTCTTTGAGC AGATGATTTG CCCCAGTGA 250
TCGTCGGC 258

(2) INFORMATION FOR SEQ ID :796:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :796:

20

TGCTTCAAAG CCTGGCTTAA CCGCTTGCC CACCAACTTC AATTATACCT 50
GCCCCTTTGC CTAACATCTC ACCGACTCGG GCAACCATCG TATCAACACC 100
25 CGCGACTCGA TCCCCATCGT AAAATGATTC CGAACTAACA TTTAACACAC 150
AATAGATAAT ACCATCAGCA TAATGCAAGG TTTTACCATC CACGACCCAG 200
AGGCGATCAA TCGCGACTAA CCGTCGTTGT AATTCAGGAC TAGCGGTACG 250
30 CTCATGTAAC GCGACAATAT 270

(2) INFORMATION FOR SEQ ID :797:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

400

(xi) SEQUENCE DESCRIPTION: SEQ ID :797:

	AAATATCGCT GCGTGCAGCT GAGTTACTAG CTGTTGAAAC TTATCGTTAC	50
5	TTGTGTAGGT TGTCTGAAAC GGTGCAGTC ACCGGTTAGC TTGATAAGTC	100
	AGGTTTTTCAG CAACTGTCAT CAAGCCATCA CGACCTATAT AAGCCACTGC	150
	AATCGCACTT TACATCATTA AGACCCTTAC TAGAAGTAAC TGGCCATCCT	200
10	GCCACCGCTT	210

(2) INFORMATION FOR SEQ ID :798:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 218 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :798:

25	ATCATAAGCG CTGGAAGTTG GGGCATTGTA CAGGGACAAC TTCGGCCTTT	50
	GTTAGCCCCA AGAGTCTACA CTCTGCCAAT GGTGCGCTCC ATAGGAAAAA	100
	CCACGGTCCA AGGCAAAAAC TACGAACCTC AGATAACCGC AAAGAGGATA	150
30	TCAACCAGAG GACGGAAATG TAAGCCTATT TTAGCCCCAA TAACGAGACA	200
	ACTAGTTGAG CTAAATGC	218

35 (2) INFORMATION FOR SEQ ID :799:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 176 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :799:

5 CCTATCAGAA TCCAATGAGA ACTACAATGG TGTGCCCAGA CGTAGAGCTG 50
AGAATAGCAT TACCAATGG AACACGTGC TACAGTCAGG ATTAAAAAGA 100
ACAATACTAC AAACCAAGTA TATCAGGCTA TTATAGCAAA GGCTGCCATG 150
10 AACAAATACAA CACTGAATTA CTCGGC 176

(2) INFORMATION FOR SEQ ID :800:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :800:

25 GCAATTGCTT AATTGTCTT TCCTTCTTAG CATTTTGCTG AGAAGCCAAA 50
CGTTGCGCCA ATTCAGAAGA TTCACGCCAG AAGTCGTAGT TACCAACGAA 100
TGGTGTGATC TTACCAAAGT CAACATCCAA GATGTTGGTT GACACGGCGT 150
30 TTAGGAAGTG ACGGTCGTGG GATACCACAA TCACTAGGTT CGGGAAATCA 200
GCCAAGAAAT CTTCTAACCA GTTAATTGTC TGCACATCCA GACCGTTGGT 250
TCGA 254

35

(2) INFORMATION FOR SEQ ID :801:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :801:

5 ATCCAGGCCC ATACCCATCA ACCCTGAAAC AACGATTGAA TCACCAGCCA 50
TTTAACCACA CATTGCAACA AACTCACATT GGGTTCCGAG CGGCAGTAAT 100
AACACAGTCG ATCAAACGCA AAATAGATGG GCAATAAGGT CGATACAAAT 150
10 AGGCAACCTT ACAATTACCA CGATCTGTAG CTATCGTATA ACCAATGAAA 200
ATG 203

15 (2) INFORMATION FOR SEQ ID :802:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :802:

GACACAACCTG TGTTCACCTAG CAACCTCAAA CAGACACCAT GGTGCACCTG 50
ACTCCTGAGG AGAAGTCTGC CGTTACTGCC CTGTGGGCTA GGCGAACGTG 100
30 GATGAAGTCG ATGGCGAGGC CCTGGGCAGG CTGCTGGCGA TCTACCCTTG 150
GACCCAGAGG TTCTTTGAGT CCTTTGAGGA TCTGTCAACT TCC 193

35 (2) INFORMATION FOR SEQ ID :803:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

403

(xi) SEQUENCE DESCRIPTION: SEQ ID :803:

5 AACAAAAGTT GAAAATTTTA AATGGTCTTT TTATGGTTTG CGTGACCTAA 50
AAAGACAAAG TTTATCCTTG CCTTACTGTA TAGAAATGCG TCGTATCCAC 100
AATAGCGTAC AGATTTTTTC GCATTAATCC GTGTTTATAT TAACAGATTC 150
10 GTTAAGTATC GTTTAAAAAG GGAGAGAGGG GATACCTCT CTCTAGATAA 200
ATGGGTCATC ATTTAATCCC AAGAATGATG TCGATAAGTA CTTTTCTAAA 250
CGATAACAAG AACCCCAGTA GGTAGTATAG CAGTCTTTAA 290
15

(2) INFORMATION FOR SEQ ID :804:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :804:

AACTTGATGG TCGAGGCCAT CTCCTGGGCC GCCTGACGAT ACCGTGGCTA 50
30 AACAGGTACT GCTGGGCCGG AAGGTGGTGG TCGTACGCTG TGAAGGCATC 100
AACATTTCCG GCAATTTCTA CAGAAACAAG TTGAAGTACC TGACTTTCCT 150
CCGCAAGCGA ATGAACACCA ACCCTTCCCG AGGCCCCTAC CACTTCCGGG 200
35 CCCCAGCCG CATATTCCGG CGGACCGTGC GAGGTATGCT GTCCCACAAA 250
ACAGGG 256

40

(2) INFORMATION FOR SEQ ID :805:

(i) SEQUENCE CHARACTERISTICS:

404

- (A) LENGTH: 286 bas pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :805:

10	AGCAACCTCA AACAGACACC ATGGCGCACC TGACTCCTGA GGAGAAGTCT	50
	GCCGTTACTG CCCCTGTGGG ACCAGACGAA CGCGGATGAA GTCGGCGGCG	100
	AGGCCCTGGG CAGGCTGCTG ACCGATTTAC CCTTGGACCC AGAGATTCTT	150
15	TGAGTCCTTT GAGAATCTGT CCACTTCTGA TGCTGTTATG GGCAACCCTA	200
	AGACGAAGGC TCATGGCAAG AAAGTGTTCG GTGCCTTTAG TGATGACCTG	250
20	GCTCACCTGG ACGACCTCAA GGGCACCTTT GCACAC	286

(2) INFORMATION FOR SEQ ID :806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :806:

35	TTCTTCATCA GATTTTACAT CTGCCTGATT AGAATCTTCT ACACTGGCCT	50
	CAGAAGATGA TTGTTCAAAA CTTTTTCTAA GTTGCTGTAA AAAAAGTCC	100
	ACGGACAAAG TAAATGCAG TTCTTTATCG TTTAGCCAGT GTACAACAA	150
40	AGGTCCAATC TTCTCTTCAT TTTAATTCAG ACTCAGAGAT GTAATAGATG	200
	GAAGAAGTGA AATGTCTGTG GCTGGGTTGA TGCTGGCTGC AATATGAAAG	250

405

TGGCAAAGTG CATTGCTATG CAGTGGAGTG TTACTGTGGA C

291

(2) INFORMATION FOR SEQ ID :807:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :807:

15 AGTTTAATCA GCTGCAATGA AAACAAACGT CTTTATTAG GCAGAATCCA 50
GATGCTCAAG GCCCTTCATA ATATCCCTTA ATTTAGTAGT CGAACTTAGG 100
GAACAAAGGA ACCTTTAACA GAAATAGAAC AACAGAAAG CGAACTTAGC 150
20 GATACTCGCG GGCCAGGGCA TTAGCCACAC CAACCACCAC TTTACGATAG 200
GCAACCTGCA CTGGAGGGGC GACTTCTCCG CCAAAGCGAC GGGCCAGCAC 250
25 ACAGACCAGC ACGTCGCCCA GGAGCC 276

(2) INFORMATION FOR SEQ ID :808:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :808:

40 GGCCTGCCAA CAGCATAGGG AAGAATCTCA TTGTTATACA TATTAAGAAT 50
CGATTCTAAA TAGACCTTTT TACCAGTCGC TGAAACTCTT AAATTAAGTA 100

406

ACATCGCTAG CTAATTTTCG TAATGGCCGA TTAATCTTGA AACGGCGGCG 150
AAGCTTGTTTTC TTCACACGTT TCCCTTCAGG TCCTTTGATG AATCATACTG 200
5 ACGTGATCGC TTATCGTA 218

(2) INFORMATION FOR SEQ ID :809:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :809:

AGCAACCCAG CGCTCAATGG TGCTAGTGAA CACAGTTGTG TCAGAAACAA 50
20 CCTCAAACAG ACACCATGGT GCACCTGACT CCTGAGGAGA AGTCTGCCGT 100
TACTGCCCTG TGGGCAAAGG CGAACGCGGA TGAAGTCGGC GGCGAGGCCC 150
25 TGGGCAGGCT GCTGGCGATC TACCCTCGGA CCCAGAGGTT CTTTGAGTCC 200
TTTGGGGATC TGTCCATTAC TGATGCCGTA TGGGCAACCC TAAGGCGAAG 250
ACTAATGGCA AGCAAGTGCT AGACGC 276

30

(2) INFORMATION FOR SEQ ID :810:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :810:

407

GACTCCACCT GAACGGGCCC CTTCTGAACC GCCTCTGTGG GAGCAGGCCC 50
CATCTGAGGA GGGTCCATCT GAGCAGATCC CTTCTCAACA GGTTCTTCT 100
5 GAGGAGGCTT ACTGCTTTTC TTA CTGATT TATTTTTCAG AGTTTCTTC 150
TTCGTACTTT TTTTAACGCA AGTATTTTGC TTTTATTCT CCTCCATT 199

(2) INFORMATION FOR SEQ ID :811:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :811:

20

AAACAGCACA ACCAATGACA GGATGCAAGA ACTGATAGGG CGCCGCAAAA 50
AAAAAGCGGG CCAAAGATGA AGTAAATAAA CGTAAGGGAG GTACCGAATC 100
25 TGGGGGGCTT GGCCTAGAGT AAGGGAGAGG AGCTTCAACT ATCTCAATAA 150
GGGCAAGAAA ACACAAACAA CTCCTTCATT CGTCCAAAAT GCTTCTGAAT 200
TGCACCACAA TTGACACACA CACACCTCAA AGCAGAATCC GCACTGACCT 250
30 AAGT 254

(2) INFORMATION FOR SEQ ID :812:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

408

(xi) SEQUENCE DESCRIPTION: SEQ ID :812:

TTTTTTTTTT AGCAATGAAA ATAAAAGTTT TTTATCAGGC AGACTCCAGA 50
5 CGCTCAAGGC CTTTCACAAC ACCCCCCAAT TTAGCAATAG ACTTCAGGGA 100
CCAAAGGACC CTTTAACAGA AATAGAACAA CAAGAAAACA AACTCAAAGA 150
CACTCGAGGG CCAGGGCCTC ACCACACCAA CCCCCTTC CAAACAGGCA 200
10 ACCTGCACCG GAGGGGAGAC TTTTCGCCA AAGCGACGGG CCAGCACACA 250
GACCAACACA TCGCCCAGGA ACCTGAAGTT TTCA 284

15 (2) INFORMATION FOR SEQ ID :813:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :813:

ATACAACAGC AGAAACAGGT ATCCACGCAC AGTCCAGCAA CATTTCTTCT 50
GGTACAACGC AGCTTCAAAG TTCACATCAA ACGTTACTTT GTCATACCAA 100
30 GGCAAGGATG CTAACGCGAA GTCAATCAGC CGAGTGATGT CATTACAAC 150
CGGTCACGGT GCCGATGTGA CAATCAAGAC TGAAGGCGAT GACGAAGAAG 200
35 CAGCACTGCC CGCCGATAAC CGCAGCGATG CAAAAAAG AGCTAGACGA 250
CTGACGAAAC CTGAGAACCC CGAAGGACT 279

(2) INFORMATION FOR SEQ ID :814:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs

409

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :814:

10 AACGTGCTGG TCTGTGTGCT GGCCCATCAC TTTGGCAAAG AATTCACCCC 50
ACCAGTGCAG GCTGCCTATC AGAAAGTGGC GGCTGGCGTG GCAACAGTGA 100
CTGAGAAGAC CAAAGAGCAA GTGACAAACG CCGAAGGAGC AGTGGCGACG 150
15 GGCGTGACAG CAGTAGCCCA GAAGACAGCG GAGGGAGCAG GGGGCATCGC 200
AGCAGCCA 208

(2) INFORMATION FOR SEQ ID :815:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :815:

30

AAACCACGCT CAGTCAGGTT CCGGCAGCAG CTGCAGCATC TCATCTTCTG 50
CGACTCTCGG TGCCCTCTCC TTCCGATTTC CGGAAACATG GCCTCCGATG 100
35 TGGCTGTCTC TGACGACGTC ATCAAGGTGT TCAACGACAT GAAGGCGCAC 150
AAGTCTTCAA CGCCAGAGGA GGTGAAGAGG CGCAAGCAGA TA 192

(2) INFORMATION FOR SEQ ID :816:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs

410

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :816:

10 GAGAGAACCC ACCATGGAGC TGTCTCCTGC CGACAAGACC AACGTCAAGG 50
CCGCCTGGGG TAAGGTAGGC GCGACAATG GCGAGTATGG TCGCAGAGGC 100
CCTGGAAAGG ATGCTCCTGT CCTTCCCCAC CATGTGAGAC CTACTCCACA 150
15 CACTTCGACC TGAGCCACGC CTCTGCCAGG TTAAGGGCCA CGGCAAGAAG 200
GTGCCCCGACG CGCTGACCAA CGCCGTGCGC ACGTGGACGA CATGCCCAAC 250
GCGCTGTCCC CTG 264

20

(2) INFORMATION FOR SEQ ID :817:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :817:

ACCCTACACA CATCCGTTCA ACTGTCCCAT CACCCACTTA CACTCCAAAA 50
35 AAAACCACTC AACAGCAAA CAACCCATCC TGTTTTTCATA ACGTTATCGT 100
AAC AAAG CCGACCATAA TCAACTGAA TTTACTTCAC CACAAGGCAA 150
AGCGATTATT TAGATGAGGC ACTCGCACTA CTGCTTGAAG TGCTACTAGA 200
40 TG 202

411

(2) INFORMATION FOR SEQ ID :818:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :818:

AGTAGAAAAT AAGTTCAAAA TTTTAGAAAT ACTGGCTTTA TACTCGCCCA 50
15 TGTATTTACA TTCACAGAGA TCTTTATTTA TTTACAAGCG CTTTGAGTTA 100
CTGTATAGTT TTTTAAACA AAAAAGCGTG GGGGGCTCCC TTAGCATTC 150
CCCATAGGAT AGGTAATGAA CTTTTTGT 179

20

(2) INFORMATION FOR SEQ ID :819:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :819:

TGTGCTCTTA TGCTAGATTT ACGGACAGAT TTTCTTCTGC CCTGTAAACT 50
35 AATAGCATAG GAGCATTTTT TAATACGATT CGATACAAA AAGAATTTAA 100
GCAATCTCTC GCCGAGACGC ACAATCAAGA CCATTCATAT ACTGATCTAT 150
CCGCTGAATA CGAACCTTCA ATCGACTCAA TCCGTAAGTG GATCAAGTTG 200
40 TACGCGGGTC CACGAAGTGA CAGACGAAAA ATGAACGCAA GCTGATGTAA 250

412

ACGCATCACA

260

(2) INFORMATION FOR SEQ ID :820:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :820:

15 ACTCGGCACT TTCTTAGAAT AGACAATTG CAAAATGTCC ATCCCAGGTT 50
CATCCTTGTA GCCTAATGTT TCCGTCACCG TTGCCACTAG TTAACGTGGG 100
TGAACCTTAT CTGGGAAACG GGTAACATCC GCGACCACAA CTAGACCATC 150
20 ATTTGACGTA ATGCCATCAG CACTCACCAA AACTTGGCCA ACCAACAGCC 200
TTTCCGTAAC TGAGTTTGAT TTCTCC 226

25 (2) INFORMATION FOR SEQ ID :821:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :821:

CACCTACATA TAGATGCACG AAGTACTTGC TCACTTTTTT TGGTTGTAAA 50
TTTCAAAGC GTTGAAGGCA GCATTCTTAG CGGCACGGAT GTCCTTATCA 100
40 GTGAATGAAT CAGGCTTTTC CATGGCCAAC CAACCAACGA TTCGCATCGC 150

413

GTGATTTCGA ATCATGTCAA GCAAAGCACC GGCTGTATCA TAGTAAC

197

(2) INFORMATION FOR SEQ ID :822:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :822:

15 GGACTGGGTG CAGTGGCTCA CACCTCACGT TACATTTTAT AGCTAGCAGG 50
GTAATGGGGA GTTATGGCAC TCAGGTCACA TTCTAGGGAA TGTTTATCGG 100
GCAATCTCAA TGGCACC GCA AGCTAAATGA CTTCCAGTGT TTCTCATCTT 150
20 TCGCGCTTTCT TCATCGCAAC CTTTGCCCAA GACATCTGTT TTTTCTGGAT 200
CACCCCTTGCA CAGCCACTGA GGAATGATCT TCTGAAAGTG AATCTTCAGT 250
25 AGACACATCG CCACACCATC TANGTCAGCC ATCACATGCC CAGGTCTNGA 300
CATG 304

(2) INFORMATION FOR SEQ ID :823:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :823:

GGCCCAGCAG ANGGAGGAAC ACTACCGAGG CTCCAGCTTA ACGGTATTG

50

414

GAGGTCAGCA CGGTGCTCAC AGAAGCCAGG AACTTGCCCA GGGAGGCGTG 100
CACCAANGGG GCGAACTCNC GGGGAGGCGG GCGACCAGGG TCACCAGCAG 150
5 GCAGTGCTTA GGAGCTGGGA GCCGACCAG CCCACCGAAC TCGCGCG 197

(2) INFORMATION FOR SEQ ID :824:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :824:

20 AAAACAATG TCATTTTGTA CAGACAAAT TTAGCAGACT CAAGCTTCCA 50
CAGTTAGTGC GAGAGCCTGT GGATGGCATA GTTACATAAG AGTCTGTTGT 100
GGATTCAAAT GTCACCTCTT CCAGGCAGTC TTTCTGACT TACCCTGGCA 150
25 GCTTTGTGTT CCCACATTAC TAGTAATGTT TTTTCCTTA ATAGCAATGA 200
TTTCACTGTA ATAATGTATT TATATGCCTC TCTCCCCCAG ACAGCAAGCG 250
30 TTTTCCACA GGTCTCGACA CACAGAAGAT A 281

(2) INFORMATION FOR SEQ ID :825:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

(xi) SEQUENCE DESCRIPTION: SEQ ID :825:

415

TATTAAATTT ACTAGAATGT TACAGTTACA AATTGGTAA TGTCTTTCT 50
GAAAAACAGC CTAATTTTGC AGCCTGAAAC TGACTGAAA ATCTCAATAC 100
5 TTTTATTCAT GATAGAAAAA TAATTCCTGG CTTCATCTCA CAATTAATA 150
ATAATTATGT TAATATAAAA TATAACTGTG CCCTTTCTTT TCAGTGATGA 200
TCAAAGTGAT TCTCCCAGGC CAAAAATCA AATAAGAAGT TATATTTTAA 250
10 AAAGACATAA CAAGCCATTC TACCCAGTGG GCATCTTCAG TGTACTCCCT 300
CTACTAATTG GC 312

15 (2) INFORMATION FOR SEQ ID :826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :826:

ACACCAAACA CGGGGAGTGG GGAGTAGAGG CTCTGGAGGT CAGGATGGCA 50
GGGCAGGGAG GGAAGGAAG GAGTTGTTGG TCTCACAGTG TGCCTGCCAA 100
30 TCCCAAAGCC CTAGAGACCC CTTCACTGCA GCACCTGCCC CCGGGTCTCA 150
GGCAGCTTCA GGGCCAGAGA GCTGCCAAGG GCAAGCAAA 189

35 (2) INFORMATION FOR SEQ ID :827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :827:

5 CTCTTAAGGG CTTGAAAATT TCTGTGGGAG TAGGACAGAG TGTAGAACGT 50
ACAGTAAAAG GCAATAAAAC AGTGGGAATA ATTTTACCAG CTATGAGTAA 100
AGGAGTAATG GGTATTTACT GCCTGTCATT AATCCACACA TATATCCATT 150
10 TTAGAGATTA TTTGTGTGCC TGGAAATCTG TCTCATCACA GAGTGTTAAT 200
ATACACCGGC GGGATATTCA AGACTGGCTA AG 232

(2) INFORMATION FOR SEQ ID :828:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :828:

25

GGACATTGGA ACACTATACT CTATTATTGC GGTCTGCCT AGCAGTCTCG 50
CGCATGTCTC CTCAGCGCGC ACAGTCTCTC TCAGAGAGCT CTTCTCTCTT 100
30 TATATGCGCA GACCCGCGA CTGGGAGACC CAGACCCAGG GCAAACCTCTC 150
TTCTTAGGTA TATCGCACCC ATCATATCTC ACACATCGTG TATGTCGTAT 200
CATCAGACCC CCATAGAGCA TATATGCTAA ATTAATGCTC TCTTTCATCA 250
35 GTAATTACCC CATATCATAA AATGCGGGCG GG 282

(2) INFORMATION FOR SEQ ID :829:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid

417

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :829:

CACTACATCC GCAAGTACAA CCGCTTCGAG AAGCGCCACA AGAACATGTC	50
10 TGTACACCTG TCCCCCTGCT TCAGGGACGT CCAGATCGGT GACATCGTCA	100
AGTGGGCGAG TGCCAACCTC TGAGCAAGAC AGTGCCTTC AACGTGCTCA	150
AGGTCACCAA GGCTGCCGGC ACCAAGAAGC AGTTCAGAA GTTCTGAGGC	200
15 TGGACATCGG CCCGCTCCCC ACAATGAAAT	230

(2) INFORMATION FOR SEQ ID :830:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :830:

30 TTCCGCAAAT AAAAGAATTC ACTAAGGTAC CAAAACAGAA AATATACAGA	50
GATCAATGAC TTTCATATAC ATTAACAAAC AAAAGTTCAG AGATAAAATG	100
GAAGAGAAAT GCTGTTTTTA ACAGTATAAT TAAGATAAAA TATGAAGGTA	150
35 TAACTTAAC AAGAAATGTT GCAAACCAT TATGTGAAAA TTACAACACT	200
CCTGAAGACG CAGACACACC TAACAA	226

40

(2) INFORMATION FOR SEQ ID :831:

(i) SEQUENCE CHARACTERISTICS:

418

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :831:

10	AGAAGTCCTT CCAAGAGTCT TGGGTATGCA ACAGCCATGG AGGCTGTGAC	50
	CTTTTTCCTT CTTTCTACA GCCTGCAGTT CATTAAAGGA TCACCGGAGA	100
	TGACTCGTGC TCTAGTTCTT AAAATCAAAC AAGGATCTGC CAAATCCAAG	150
15	ACCCTGAATT TGGCCCAAAT TTGTAGAAAC ATTGCTTTTT ACCACCCGGT	200
	GCACCAAAAA TACCTCCCAT TTCAAGGCAA CAACCGCTTT AATTGCT	247

(2) INFORMATION FOR SEQ ID :832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :832:

30	CACCAGGCAG GGGATCCCGG AGGGAAGCCC TCTGCCAGGG ACATGGTGAG	50
	GGCGTGGCCA TCACCCACGA AGGGAGCATA AATAACACTG GCAGGTGGGT	100
35	GGGCAGCAGG AG	112

(2) INFORMATION FOR SEQ ID :833:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid

419

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :833:

AGCCATTCCC ACTAGAGGCC AAACCGCCTG CCCACAGAGA TTGACAGCCA 50

10 ATGTTTCATCT CATAACTCTC CTCCCAGCAG TGCACCAAGTA AACTCAGATG 100

CCTGAGTGCT TGTGGCCACC ACACAACAGA TCGGGCCTTC CTCTTCACTG 150

15 GCCCCTCGGC TGCTGCTGGG TCC 173

(2) INFORMATION FOR SEQ ID :834:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 288 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :834:

TGGCCCATGG GAGCCCTTAT GAGCAAGTTT CCAGGTCCTT ATGACACAAT 50

30 TCCATCATTG TTCGGGTACA TCCTTACTCT CTGGCACAGT AGAGATGTTC 100

CAGACTTATC TTATATTTTC ACTTCCCAT ACCTGGAATC AATCACTTCT 150

35 CCGAGGATGC TTGATTCCTT TTAGTGAAGA ACAGTCTTTG GAAACCAACC 200

GTCTAGGGAC ATCAAGTATG TTTGCCGCTA TTGGAGTGTC ATTGCTCCTG 250

AACCTTCTAA GTGGACACAG CTAGGAAATG TATGTGCT 288

40 (2) INFORMATION FOR SEQ ID :835:

(i) SEQUENCE CHARACTERISTICS:

420

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :835:

10	CTTTTCTATT TTCCTTAAGT GTCTGCCAGT CTGAGAAATA AAGGGACAGA	50
	GTACAAAAGA GAGAAATTTT AAAGCTGGGT GTCCGGGGGA GACATCACAT	100
	GTCGGCAGGT TCCGTGATGC CCCACAAGCC ACAAACCAG CAAGTTTTTA	150
15	TTAGTGATT TAAAGGGGA GGGAGTGAC GAATAGGGTG CGGGTCACAG	200
	AGATAACGTG CTTACAAGA TAATAGAATA TCACAAGGCA AATGGAGGCA	250
20	GAACGAGATC ACAGGACCAC AGAACTGGGA CCAAATAAAG ATTGCTAAGA	300
	ACGTCTAGGG	310

(2) INFORMATION FOR SEQ ID :836:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :836:

35

	TCAGTGGAGG AATTAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT	50
	GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA	100
40	GAGGTAATCA AAAACTTGAG CATGTATTTA AGGATCCATG ATTGAATTTA	150
	CATCTCCCAA AATGCCTAGC ATTCTTC	177

421

(2) INFORMATION FOR SEQ ID :837:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :837:

CCGTTGCACT TGGTGTGGC ATTCTGCAGG GCGGCACTCT CCCACTCTTC 50
15 CCGGCCTCGA GCCAACCTGA CGGCAGCCAG ATGGCAGTCG TAGTGCACAA 100
TGTGAAGTG GGACACGGTG CTGTAGCCCT GCTGT 135

(2) INFORMATION FOR SEQ ID :838:

20

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :838:

30

TCAGTGGAGG AATTAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT 50
GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA 100
35 GAGGTAATCA AAAACTCGAG CATGTATTTC AGGATCCATG ATTGAATTTA 150
CATCTCCCAA AACGCCTAGC ATTCTTCGCC ACATTACAGT AGCAACATCA 200
G 201

40

(2) INFORMATION FOR SEQ ID :839:

422

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :839:

10

TTCTTTGGAG TACATCCTTA CTTTCTGCAC AACAGATGAG AGATGTTCCA 50
GAACTTATAC TGTATCATAT ATTTTACCTC CCCCCCTATA CACCCTGAGA 100
TATACATATA CACTATCTCC GCTAGAGAGA TGTCTATGAC ATATCACTTT 150
CTGAGATGTA CACGAACGAG ATCTTTTGAG A 181

20

(2) INFORMATION FOR SEQ ID :840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :840:

30

CATACAAATG ATTAGAAAGC AATACAGCCT TATTGCTGAT ATGGAGAAGG 50
TTTTAGTGAA CATTGAGAGG AGTTTGAAG AAAGTCGCTG CACAATCTTC 100
ATGGATGACT TTGAGGGATT CAAGACTTCA GTGGAAGAAC TAACTGCATA 150
TGTGAGTAGA AATGGCAGGA GAACTAGAGT TCGAAGTAGG AGCTGGAAGA 200
TAATAACATG GGTTTAAAAA AC 222

40

(2) INFORMATION FOR SEQ ID :841:

423

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :841:

10

CGCTCAGCTG GTCTATCCTG CTCTTCCTCT TGTCCCTGCT CTTGCTGCGG 50
CTCCTATCTA CCGGCTACCT GGTGCCCCGCT TTGCTCCTGC TACCGGCTCC 100
GACTCTGGCG GAGGCTCTTC TCCTGGCTCC TGGCCCTGCT CACAACCTCC 150
TCGCTTCTCC TCCTCCACTC TCCTCTCCCG ACTCCTGCTC CGACTTTTGC 200
TCTTACTTTT ATGCCTGCTA GGACTCCGGC TCTTGGGTTT CCCGAACATT 250
GTCATTGTTT TGGAATTCT CCTTCAGCTT GGTCTTTTGC CGG 293

20

(2) INFORMATION FOR SEQ ID :842:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :842:

35

ATGAGGAGGT GAGGAAAAGG AGAAGTGCAG CTACCATCGA GTGATTCTTC 50
TGGGATAGGT GTCTCATTTA AATCTCATAA TCATCTTTT TGGCAGGTCA 100
GTCAACTCA GGCTCACAGA TGACAGACAG TTGGCCCCAA GACACACAGG 150
AAATACATAA GTGACAACGG AATACAAGTC CATGAATTAA AAAACCATGC 200

40

424

TTTTCTCTCC TTGCCACACA GCTTTAGTTT GAAAAA

239

(2) INFORMATION FOR SEQ ID :843:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :843:

15 TTCCGAATTA TTGAATCTTC TTCTGTAACA TCACAATCTT CCTGGTTTTC 50
AGAATAAACG CTCTTCTCGC TGCCTCTCT CTGCACTCAC TCCCACCTCA 100
CTCACTCACT CTATAATAAA ATGTTTGCAC TCAATTTATA TAGTAGTGTT 150
20 TGTC 154

(2) INFORMATION FOR SEQ ID :844:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :844:

35 GTCTTTAATT GAGAAAGCTG GAGTGGAGAC CCGATCCCCT GGGAGCAGTG 50
CCAGGAGTTG GGTGGAGACT GAGTGGGGTT TGTGTGGGTG AGGGGGCATC 100
TACTCCTCTT GCAACAAGCC AGAAGTAGAA CAGCCTAAGG AAAAGTGACC 150
40 TGCCTTGGAG CCTTAGTCCC TCCCTTAGGG CCCCCTCAGC CTACCCTATC 200

425

CAAGTCTGAG GCTATGGAAG TCTCCCTCCT AGTTCCTAG CAGGTTCCCC 250
ATCTTTTCCA GGCTGCCCCCT AGCACTCCAC GTTTTCTGA AAAAATCTAG 300
5 ACAGGCCCTT TTTGGGTACC TAAAACCCAG CTGAGGTGT GAGCTGTAAG 350
GTAAAGCAAG TTCTATCCAA TTAGAAGCTG TTGGGGGCGT AT 392

(2) INFORMATION FOR SEQ ID :845:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :845:

20

CAAAGAATAA ATAATTTTTC TATTCCTGAA AGTAACTAA TTATTTATTA 50
GAAAGTCAGA AATATGTGGA AAGCAAAGGA ATATTTGAGA AAGTGATATG 100
25 AAATTAATAA GTGGTAAAAA ATTAATAAAA TTAATATTAG AGTTCCTTT 150
GAGCTAATCC TTTATTTATT TATTTTTTTC CTTGAGACAA TGTCTTGCCA 200

(2) INFORMATION FOR SEQ ID :846:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :846:

40

TTAAAAATAC TCTGGAAAGA GCACTTCCAT CGTTCATTTA CATCATATTA 50

.426

5 GAAATGGATT TCCGAGTCAG CACTGGCTTC CTCCAGAATA GCAGTCCTGG 100
 AGGAGCGAGA TCTCCCAAG CCTCCAGGAT TGCAGTCTGT TTGTGCCTT 150
 10 CACTCCCTAA TAGGTTTGCC TTATTTAAAG GACCCACCTT CAGAGCTGCC 200
 AAGGACTTTC TCAGAGCAGC TCCTTGGTCC CTCCGACAGC CTGGGATGGC 250
 ATTTATTCTG GGGCCTGGGT GTGGGGAGGT CCTCACCAGC CTAGGAGTAA 300
 15 GAGGAGGTGG T 311

(2) INFORMATION FOR SEQ ID :847:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 287 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :847:

25 CAGATCAAGA CTGGTGCCCC TTGCCGATCT GAGCGCTTGG CCAAGTACAA 50
 CTCAGCTCCT CAGAATTGAA GAGGAGCTGG GCAGCAAGGC TAAGTTTGCC 100
 GGCAGGAAct TCAGAAACCC CTTGGCCGGG TAAGCTGTGG GCAGGCAAGC 150
 30 CCTTCGGTCA CCTGTTGGCT ACACAGACCC CTCCCCTCGT GTCAGCTCAG 200
 GCAGCTCGAG GCCCCGACC AACACTTGCA GGGGTCCCTG CTAGTTAGCG 250
 35 CCCACCGCC GTGGAGTTCG TACCGCTTCC TTAGTCT 287

(2) INFORMATION FOR SEQ ID :848:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

427

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :848:

GATTACAGGT GTGAGCCACC GTGCCTGGCC TATTAATATG CTCTTAAAC 50
TCATCCATAC GTTTTCATAG CAAGAAAGCT TATTTCTCCC AACTACCGAA 100
10 TAATATTCTA TCGTATGGCC GCACCTCTGT TTATCCATTT ACCTATCGAG 150
AGGCATCTTG ATTACTTCTA GCTTTGGATT ATTACAAATA AACTATACA 200
15 AACACGCAA CAGAGTTTCT CGTGTGAATA TAAACCCGCA AACCGGCTGG 250
AGGCATATNA CCA 263

20 (2) INFORMATION FOR SEQ ID :849:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :849:

TTGTCAGTCA GAATAGGATG TAAAGACTA TTTCAAAGAG TTAAATTATT 50
TGTTAATATC AGAGATCAGC CACAGACAAG AAGTTTATGG ATGAGTGCAG 100
35 CAGTGGTCCA TTGGACATGT TAAATACTCG TGGATATCCA CAATTCGAAT 150
TGACATTAAA AACGAATGGA TACCCAACCTC TGAATTCCAT ATCGTTTTTT 200
AATATCAAAA ACACAATTTT AACTACTGAT AAACCAGGCA ACCACCGCAA 250
40 GTTTATCGAA ATCCTGCCGC TACTAAACA 279

428

(2) INFORMATION FOR SEQ ID :850:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :850:

GCTGAAAGTT GAAGTGGAGA GCTTGAAACG AGAACTCCAG GACAAGAAAC 50
15 AGCATCTGGA TAAACATGG GCTGATGTGG AGAATCTAAA CAGTCAGAAT 100
GAAGCTGAGC TCCGACGCCA GTTCGAGGAG CGACAGCAGG AGACGGAGCA 150
TGTTTATGAG CTCTCGACAG AAT 173
20

(2) INFORMATION FOR SEQ ID :851:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :851:

TCGAGAAAGT TTCAATGTGA TTAGATTAAA ATTAAAAGAA TCCATAAAAA 50
35 TGAACAAAG AAGAAGAGGA ATGAAATTAC TTTTACTTTA AACAGCATTG 100
TTATCACATA AAACACGTAT CTTACAAATT CATGGGATAG CCCATAAATG 150
GGACTACAGC AACAAATGGTA GGAGAGTCCA TCCTTCTTCA AAAGCAACCC 200
40 AGCAGGAATT TTCTGTAAA AATATTTTGT CCGTAATACT 240

429

(2) INFORMATION FOR SEQ ID :852:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :852:

ACTGGACTGG TCAAGAACAA AGCTCATGGC AATAGTCTTT TGGAAATGTTA 50
15 AAGGAATTTT TCTAGTTGGC TTTCTGGAGG GCCAAAGAAC AACAACATCT 100
GCTTATTATG AAAGTGTTTT GAGAAAGCCA AAGCTTTAGC AGAAAAACAC 150
CTGGGAAAGC TTCATTAGAG AGTCCTTCCC CATCACAACG CTTCTGCTTA 200
20 TTCCTCTTAT AAAACAAGGG CAATTTTGTG AGAGCTACTG ACGATTTTCC 250
CCTCGAAATT TACTATTCTT ACAGCTTATT AATCTCAAAT AGTAAGCATG 300
25 TCCTTGCCGT CACT 314

(2) INFORMATION FOR SEQ ID :853:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :853:

TCCTGAAATA CTCTCTACTG TCACTGCTTC AGTTTAATTT ATAGATAGCA 50
40 CCAGATATGA GTCCTTATTA GTTCTGATAA CTCTGAAATG GTTATTTGGT 100

430

ATTCTTCAG TGACAAGCAA ACTATCCCC CACATGCCTT TAATGGCCAG 150
TGTTTCGAT TTGTATACCA ATAAGCAATC TAGGTAGAGG TAATCATATA 200
5 CTGATACGCT AACCTTTGAA ACATAATTTC CAATCTAGTA AGCTAAAATC 250
GCGCCAATAC TGCTTAA 267

(2) INFORMATION FOR SEQ ID :854:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :854:

20

GCAGTGGATC TTTCTTTTTT TCAAAGGAA ATTCATATA GAGTCCATTC 50
ATAGGAAACA GATAAATGT GAACGGCTGC AACTGAGATG GGGGAGAGTG 100
25 GCTTGGAGCC CCCAGCCTCT TTGCTTCTC TTATCCCTAT AGGATGGCCA 150
TTAGGTGAAG CAGTTTAGCT TGTGGTTCA GACCTG 186

(2) INFORMATION FOR SEQ ID :855:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :855:

40

ATTTGAAAA GAAACCTACA AAAATTGTAT TTCCATATT CATAGTCAGC 50

431

CAAAAATATT GGTCAACTCA TGCTCTCTGC AAGGTTCTGC AAAAATTGCG 100
GAGTGGTATA GACAAGGCAC CATTGCAATA TATAATACTT TTTGGGTATT 150
5 GGCCCAAAAA TT 162

(2) INFORMATION FOR SEQ ID :856:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :856:

TCTGTGGCCA CAGATGCATA TTACAAGCCC ATCCAGAGCC ATTATGAAGA 50
20 GAAAGTGGCA ATTTTATTCT CAGCCTGAGA AATCCACACC AATCTAGTCT 100
GGGTTTCCAA GGATCTGCCG TTAAAGTCAC TTAGCCTCTA TCCTTTCCGG 150
25 GAACAACCTG CCCCTAGAGA GGGTGAACGA GAATCGTCCC CAGTGCCTCC 200
AACATAACAA ACCCAATCGC CCTGTAACT TTAAATCTTC AACTCGAGAA 250
AAAGGCTCAT GACTACTTCT AACCATGCCC AAACCC 286

30

(2) INFORMATION FOR SEQ ID :857:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :857:

432

AACTATATGG TATTATTTCA CGCTGTACCC AGTCCATTGC TTGAACTTAC 50
 GGGTACCTAA TGAAACGTGG AGGTCCGGAT GTATGAAAAT CTCCTCTTTT 100
 5 CCCCTTTACT TACAGCCTCT GTAGGCAATA ATTATAGAGT AGTATAGATG 150
 ATTTTCTTT TTTATAAATC TGCCTATCTC CAGGAGGATG GGGCGCGCAC 200
 TTTTAGAAAT GCATATAAAT GCTCTACGCT CCTTTTTTCT GTTACTTAAT 250
 10 CGGCGCCAAG GCCTTTACAT GAATACTCAG 280

(2) INFORMATION FOR SEQ ID :858:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :858:

25 CACTGGTTTT CATGACTGAT TTCTTTATTT TTAGTAGTTC TGACATGTTG 50
 GCCAGGCTGG TCTTGAATC CCAGCCAACC TCAAAGTGCT GGGATTACAG 100
 CTGTGAGCAC CAGCCCAACC TCGCCTCTTT AAAAAGAAAA AACACAAGTC 150
 30 CACTCTGAAG TCAGCCTCTG TAACCTCCCC ACAAGAAAAC CGTTTACAT 200
 CAGTCACTAA CCAAACAACC AACAGTGCTT CAACACAGAA AGTAAAGCAT 250
 35 TATACAGGGC TTGAACTGTC TTTAAGCAA GCCCCAAATC CTTTGAAAGG 300
 AGGCAGTAAC 310

(2) INFORMATION FOR SEQ ID :859:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 base pairs

433

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :859:

	TCTGTGTGGA GGGGAGGGAC CCAGTCTGGA CCCAGGTGTC ATCATCTCAG	50
10	CCACAGCAGG GCCCTCTCAG GCTGGGAAAC TTCTGCCAGA GCTGGCGAGT	100
	CCTCTGCAGG TCAAGCCAGG GCTTGGACAC AACTACTTCA TCTATCGCGC	150
15	AGGAAGAG	158

(2) INFORMATION FOR SEQ ID :860:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 263 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :860:

	TTTCTAATAA GAACATAAAA TAAAGGCTAA TTAAAAGAAG GTGACTGAGT	50
30	CCAGGAAGGC ACTAATCAAA GATGATATAC AGCCAGGTAA AAAAGAACAA	100
	TTACAGGCA CAAGACTATA TAACCATCGT TTTATTTTCA AACGTTATAC	150
35	AAAATATACT CTACCGAACT ATAATAGATC ATTAATAGTG GCACAATCTT	200
	TAGATTCGGA ATAACTTGAA AATAAATCCC AACCACGTAA CTTACTAAAG	250
	GAATAATGAG CCA	263

40

(2) INFORMATION FOR SEQ ID :861:

434

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :861:

10 ATTTGTCTGA AAAATATATT TCTACACGAT CTGATAAAGT TCAGATAAGG 50
 GGCATTCTAT TCCTAAGAAT GTCCTAAAAA TGGAAACTG ATAAAAGATT 100
 15 ATGCTTAGAA TTATACAGGT AAAAGACCTA CAACAATTGT TCTCTTGTTT 150
 TGATCCCATATA GGTCATTTGT TATTACTCTT CTTCAACAGA GTGATTTTCT 200
 ATTATAAACT TTCTTAGGAG CCAATACAGA GTAGAAAGAA ATATTTTCAG 250
 20 AAAG 254

(2) INFORMATION FOR SEQ ID :862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :862:

35 G TTCCTCCTT TGTAATTAT GAAATATTTA TAGTTTAGAC TGAGTAATAT 50
 GACATGAAAC AACAAACCTG CACATTTCTA ATTTATAACA AATCCGTTTC 100
 CTTAATGGGT GGAAGGAAAT CTGAGGACAA TTCTAAGGAG TCTTGCTCTGC 150
 40 TTTCAGTGCG ATCTTCTAGT CATACTGAAG ACAATACCTC TCCAGATTGA 200

435

TCTTTCCCCT TCTTATACTC TTCCCGATCA ACGTCAATCA CACGCACCAC 250

TCCAGGTTTT AGACTTAGGT CATCCGTCTC TACCTGACTT CTGTTGCCCT 300

5 TCACCTACAC GTGGCTCGCT TTAGTTTGCT GAGCAGC 337

(2) INFORMATION FOR SEQ ID :863:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :863:

TGGTGGGTTT GAGCCCAACT TCAGCGCTCT TCGAGAAGTG CGAGGCGAAC 50

20

GGTGCGGGGG CGCCTCTCCT CTCCACCTTC CTGCGGGAGG CCCTGCAAGC 100

TCTCAGCGAC GAGGCCACCA TCTTCTGACC AACTTCAGGC TACTACCCCA 150

25

ACTTACAATG CCACCGCGA 169

(2) INFORMATION FOR SEQ ID :864:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :864:

ATTAAGGTAA AGGAAGACTT TCCATTGTGA ACTAGAAAGA GTGTCCTGCT 50

40

ATTACTACCA TTCACATCTA GTTGTGTGA ACTAGGGTTT TCTATCTTAA 100

436

CCCTGTAAA AACAAAGGAA AGAAATGGGC TGAATGGCGC ACCAGCTATG 150
CGGATAGCAT TATCTTCCTG TGTCCAGAC TGAATGAAT TTATGAACAA 200
5 GGCAAGCACA CCATTATACT AAATAAAATC TTACCTAGTT TTCGTTTTTG 250
CATTTCTTAC TTCGCAGTAT TTCTCCCGCC AAGAGC 286

(2) INFORMATION FOR SEQ ID :865:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :865:

20

ATATAGTCCG CTAGGGATAG TGAAAATTT GGGGCTTGGT TTAGATTGGA 50
GAGGTATATG GTGGGGTGTC TTATAAGGCT TAACTTTGGG AGGGCCCAGG 100
25 GCCTTGATTT CTGTCCCCCT TGCCTTGCGT GGCCTTTGAA TTGAAAGCTT 150
TGAATTAGGC CTTCATAGAT TTAGTGTGC ATACAAATAA CACGATCTTT 200
TTATAAGGCA GATTATGATT CTGAAGGTTT AGTGTGGGAC CCAAGCTTTC 250
30 GCATTTCTGA TCTATAAGGT GA 272

(2) INFORMATION FOR SEQ ID :866:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

437

(xi) SEQUENCE DESCRIPTION: SEQ ID :866:

ATGCAGGAGA AGAAGGATGC CAACTAAGT CAAAAAACG GAACGCAAAT 50
5 AAAAGGAATG AGCACGGTTA CAAAGTCACA GGATGAGTCC CTGGGATCTG 100
GGGCGGGAGA AGGGGTGAAT CAAGAATGAC TTGAGCTTGT TACTCCCTAG 150
CAGGCTGAGG GCGTGACACA GCAGCTCGAT GACAAAGAGG TCTATTATAG 200
10 TTTCTAACAC TACAACGCTA ACTTTTGAA CGTATCTACT TCTAGCATGT 250
AGACAGATCT CTAATCGCCT GCCAGACGGT AAGCCGCAGG AATGCG 296

15 (2) INFORMATION FOR SEQ ID :867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :867:

TATTTTATCT CAACATAATA AAAACGACTA TAAATCTTCC TAAGAGAATG 50
CTCTACTCCC AAGACTAATT TAAACTCGGG GATCGTCAGA GGGAGTGCCA 100
30 CTGTGACTTC TACGATGAAA GAACAAGGGA GAGAAGATCT TATCGACAAT 150
CATACAAAGC CATATATACG CTATTCCTCA ACTCACAGAG TTAATTAAAT 200
35 GTCACCAGGA TGGAAGAAAC CTTATAAGCC CCTATCTATC A 241

(2) INFORMATION FOR SEQ ID :868:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

438

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :868:

GGACGACTGC AAGCTGGAAC TACACACGCG CACTCGCTCA CACTACACAC 50
ACGCCACTCT CACACACTCT CACACACGCA CCCTCTCGCG CATGCTCTCT 100
CAAAGCCCAA TATAACCAAG GGGAAGGAAT 130

(2) INFORMATION FOR SEQ ID :869:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :869:

25 TTCAAATATT TATGTATGTT TGAACATTTT CATAATAAAA TGTGAAAAA 50
CTAATGAGAA TGGCATAAAC AACATTTAAG CAATATATTT TGAAATTTAA 100
TTCAAATGGT CAAATTCCTG GAAAACACAA ACTCCCTTCA CTAACAGAAT 150
30 TGATAGAAAA TCTGAGTAGT TCACCATTGT TAAAGAAATG GAATGTGCCA 200
TTTAAAACCC TCCAATTGAA AATACTACAT ATAGTTACAA TAGGGAATTT 250
TCCCAAGCAC TTAAACAATA AACAAATGCCC TCTTTATACA AACCTTTCCC 300
35 AGTAATAGAA 310

(2) INFORMATION FOR SEQ ID :870:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs

439

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :870:

10	AAAGAGGCAA GTTCCTGGTG CAAAGGTGGC TCTGCAGCAT AATTTAGGCA	50
	TTGGAGGAGC TGTGTGTTGT AACACTCTAC AAGATGGGTT TTCCGGAAGC	100
	CGCCAGTTCT TTTAGAACTC ATCAAATTGA AGCTGTTCCA ACCAGCTCTG	150
15	CAAGTGATGG ATTTAAGGCA AATCTTGTTT TTAAGGAGAT TG	192

(2) INFORMATION FOR SEQ ID :871:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 250 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :871:

30	ACCATAGATG TGTTCCAGAG GCAAAGAGA CACATTATCC TAGATGGCAG	50
	AACATGCTTT CAAACATAT AAAACGTCAA AGTTCCAGAT CTTTCTACAT	100
	TTTAAATCCT GTCTGAGGAT GGCAGCTGAC TTTATGTAGC TGATAGACGA	150
35	CTAGAGTTTC ATCCAAATAC CTGACCACGA CTTTCATGGAG ATTTGAATAA	200
	TCTATCCGAT GAGATTTATA TNTAAACAAC TCAACTCCTG TCGAAACAAA	250

(2) INFORMATION FOR SEQ ID :872:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs

440

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :872:

	TCAGCTACGA ATTGCTTCCT TCTCACAGAA CTGTGACATT TATCCAGGGA	50
10	AGGATTTTGT ACAACCACCT ACCAAGATTT GCGTGGGCTG CCCCAGAGAT	100
	ATACCCACCA ACAGCCCAGA GCTGGAGGAG ACACTGACTC ACACCATCAC	150
15	AAAGCTTAAT GCAGAGAATA ACGCAACTTT CTATTTCAAG ATTGACAATG	200
	TGAAAAAAGC AAGAGTACAG GTGGTGGCTG GCAAGAAATA TTTTATTGAC	250
	TTCGTGGCCA GGGAAACACA TGTTCCAAGG AAAGTAATGA AGAGTTGACC	300
20	GAAAGCTGTG AGA	313

(2) INFORMATION FOR SEQ ID :873:

- | | |
|----|-------------------------------|
| 25 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 270 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |
| 30 | |

(xi) SEQUENCE DESCRIPTION: SEQ ID :873:

35	TAGATGCTGA TGGCAATGAC ACAATTGACT TCCCTGAATT CCTGACAATG	50
	ATGGTAAGAA AAATGAAAGA CACAGACAAT GAAGAAGAAA TTAGAGAAGC	100
	ATTCCGTGCG TTCGATAAGG ATGACAATGA CTATATTAAC GCTGCAGAAC	150
40	TTAACCATAC AATGACAAAC CCCGAAGAGA AGTTAATAAA TGAAGAAGTT	200

441

GATGAAATGA TCAAAAACGT AGATNATTGA TGACGATGGT AAGGTAACT 250
ATCCAGCGTT AGCACAAATG 270

5 (2) INFORMATION FOR SEQ ID :874:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :874:

TTGGGCCATG TCCCCATTTT ATCTCCAAAG CCAGCCATGG TGTATTCTC 50
TCTGCTTTTC TTCCATATTT CCAACCCAGA AATGACTCCT GTTCCCATAT 100
20 GTGATTATTA TATTGCGCTA ACCCAAGTGA TTAAGGATAA TCTCACTACT 150
TAATGACAGC TGATTATTTT CATCTGCAAA CTTACTCAAG AATGCAATCC 200
25 AGACTAACAC GACAATAGGA CATCAAGCT 229

(2) INFORMATION FOR SEQ ID :875:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :875:

TTTGAAC TTT CAGCCGAATA CATCTTTTTC CAAAGGAGTG AATTCAGGCC 50
40 CTTGTATCAC TGGCAGCAGG ACGTGACCAT GGAGAAGCTG TTGTGTTTCT 100

442

TGGTCTTGAC CAGCCTCTCT CATGCTTTTG GCCAGACAGA CATGTCGAGG 150
AAGGCTTTTG TGTTCCTCAA AGAGTCGGAT ACTTCCTATG TATCCCTCAA 200
5 AGCACCCTTA ACGAAGCCTC TCAAAGCCTT CACTGTGTGC CTCCACTTCT 250
ACACGGAAC TGCCTCGACC CGTGGGTAAC AGTATTTTCT GCGT 294

(2) INFORMATION FOR SEQ ID :876:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :876:

20

ATTTTGGTA ACATACATCA AGTGGCACTA ATTACACAGT AACTATAAGG 50
TAACTAACAT GAAACCACAG AACTGTAACT CTGCCACAGC TGCATGAACT 100
25 CGGGTTGTCC TGACCGAGCC CATCCCCAAA AAACCGCCCA CCCCAGAGCT 150
ACGCCAACAA AAACCGTTAT TAA 173

(2) INFORMATION FOR SEQ ID :877:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :877:

40

TAATCAAAAG AGCTCTAAAT CTGTAATTTT TTTCTCCTTT AAAAAAATGT 50

443

CTACTTTGTT TTGGTCCTAG GCATTAGGTA ATATAACTGA TAATATACTG 100

AAACATATAA CGGAAGATGC AGATGATAAA ACTAATTTCG AAC 143

5 (2) INFORMATION FOR SEQ ID :878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :878:

ACTGAATAAA CTGCTGATGT CCAGGTTGAG TGGTTCCTGC TGTGGGACTT 50

GCGTTTTCAC TAAGTGTGGC GTTAGATCCA TTAGTTCCCG AAGAGCCTCC 100

20 AGTGCTTCCT AATGCCCCCA AGCCAGGAGT AAACCCTGGA ATGAGGCCCA 150

GGGCTTCTAT TGCTAATGCC TGTAACCTT GCTGAATCTA TAACAGAGTC 200

25 TATACCGCTC TCG 213

(2) INFORMATION FOR SEQ ID :879:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 227 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :879:

AAAGAAGGAA AAGAAAGAAA TAACACTTAA CAGTCCATAA CAAAGTGTTA 50

40 ACGAGATAGA CACATGCTTA TTCAAACCAC AGATATGATC CAGTTAATTC 100

444

CCTTCTTAGA ATGTGCCCAT AGTGCCTTAT TGCCTCATAA TAATGATAAT 150

AATAAGAGCA ACAATAATAA CGGCACAAAC TCCAGTCGAT ACTGACAAAC 200

5 TACCAGAGTA ACCGTCATCC CCTTGAG 227

(2) INFORMATION FOR SEQ ID :880:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :880:

ATAGACAAAG TCCTTCCCAC TAGAACTTAC ATTCCAGTGG GAAGAATTAG 50

20 AAGCCTCAGG AATTCCATTG CTTACTTTTA GTTGTTACTT CAAAAGTACT 100

TACATTTAAT CTGATTATTA ATTATTCGTC ATGAGCTTCA TTTTATTACA 150

25 TCCAGGGCAC AGTATGTGAA TTGTGTTTCG TTCCTTTAGG AAAAGGAAAA 200

ATAATCACTC TTTACAAGGT A 221

(2) INFORMATION FOR SEQ ID :881:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :881:

40

AATTGTGGTA TATTCATTT AAAATCGATC AAAGACAGCA ACATACATTA 50

445

ATCAGAGGAA AGCATCAATT AAATGCAGAA ACAAGATTTA AACAAAGATT 100
CATATTAAAA CAATGATAAG TAATACTTAG AAAGTGCATC CTAGAGACAC 150
5 ATCATTTCGCA TTTTGTAGAA AACAGAAACA TATTAGTGTG AAAAGATGTT 200
AAAAAATGAA TATTAAACCG TCGAGCACAA CACACTACGC CGATAACAAT 250
ACACCACAAG CGCCGTAATC CTGCCGACAC TGACACACTA CAGGCGTCGT 300
10 GGCGATCCGA 310

(2) INFORMATION FOR SEQ ID :882:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :882:

25 GTTCACATCA GTGTGTAGGA TATGCTATCA CGTATGTGCA TGAGAAGAAT 50
GGAGAAAATG GATCTATGCG GATGTCTGTA CACACACACA CACACACATA 100
CACAACAAGC TTGCACATGT ATAGAGGATC CGAAATTCCA CCAATACTGA 150
30 CGAACTACAA ACGTAACAGC AGCAGGC 177

(2) INFORMATION FOR SEQ ID :883:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

446

(xi) SEQUENCE DESCRIPTION: SEQ ID :883:

CAATTCTATT TTCAGAGTTG ACTGTACTCT TTTCCTCTGA AGATACACGT 50
5 ATAAACGCGA CCAACGAGGT CTCTCGTCCT AATAACAGGT TCAGGCATGA 100
ATCACCGTCT AACAGCTATT TAAACACCGC CTCTTCATAG AAGTAACGCC 150
GA 152

10

(2) INFORMATION FOR SEQ ID :884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :884:

CCATAATATA AGTATTTATC ATGTATTCTG TGTCTGGAAT ACAATTCAAT 50
25 GACCTATTTC AGAAAAATCT TTTCAAGTAC TGGCTGAAAG AGTGAGGGAT 100
ACATTAGGAG ACTGCAAATA AACTGGCAAT CACAAGAACT TTTTCGGATA 150
AAATGAAATT GTGCCGAAAT GTATACA 177

30

(2) INFORMATION FOR SEQ ID :885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :885:

447

CACAGCTGGA AGAGCGGAGA AATAGAATTG TCTTCAAACA ATATAAAAAT 50
TCATAAAGAA TAGAAAGACT ACTATGTGTG GGTCGGGAAA TTAAGTAGAA 100
5 TTTTTTTATA TCCACACTCT AGTATGAAAT GAGTACTTAT AGAGTAGAGT 150
GTAACATATT TAGACATAGT ATATATATAT ACAAGTGTAA CAAATATATA 200
TATTAAATAT ATATATGTTT TATAGAAACA CAGAGCACAC A 241

10

(2) INFORMATION FOR SEQ ID :886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :886:

GTAGCAACCG GCGCTCAATA AAATTCAACC AGCAAACCTCG ACAAGTAACA 50
25 ACCATAAAAC CAGCCACACT AAGTCCAGCC ACCACTACTC AATAAAAATA 100
ACACGTATCT TCCACCGTAC AACCAATAGC AACTGCAGGC TACTGCAACG 150
CCATCCATAT ACCAAAAATG CTAATTACAA CACCACAACA 190

30

(2) INFORMATION FOR SEQ ID :887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :887:

448

5 CACGCTTTCT CTCACACAGC ACTAGCGCTC TCTCACTATC ACTCTTCTCA 50
CAGAGCTGCG CGCGAGTCTC ACTACTATCA AATATATCTG TCTCTTCTCA 100
CTCTATAGCT CTCTCACAGA TATATATCTA CATATAGCGC TCTCATTATA 150
CTATAATATT ATACTCTC 168

(2) INFORMATION FOR SEQ ID :888:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :888:

20

ACTGGGCGCG CTGGTGCTGA CATCTTCAAG AGCATCTGTC ACTGAATATT 50
GCCGATCTCG CAACCGGTTT CAGTTAGACA GAACATTGTG ATATTCAAAC 100
CACTTTCTCG TAATTTCCTA TGGAGTTGTA AAGTTTAATG AGACCTCGAT 150
AATCATATTC TAGTCCACTG TAGC 174

25

(2) INFORMATION FOR SEQ ID :889:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :889:

40

ACACCACACT TAAGGAATGG GAGTTATATT TCACTTCCCT GAGGCCAGAA 50

449

TATATATATG TATGTATGTA TATGTGTGTG TGTGTCTATA TATATATATA 100
TATAGACACA CACGCACATT ATACACACAT ATATATACAC ACACATATAT 150
5 ATATGTGTGT GTACAATATA TAAAAATTA TATGGGAGAA AAGAAAGGCA 200
AATCTCCCAT GGCAGAGAGG TATCCCAAAA AATTTTTTTG TGTGTAACAA 250
AATATGTTGT GTGTATATAT ATATGCACAC ATATTTATGT GTATATATGT 300
10 ATATATATAT CTGTATATAC AGGTATA 327

(2) INFORMATION FOR SEQ ID :890:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :890:

25 TTTTTTCTT GTCTCTCCCG CAGCGCGCGC CTCTCGCGGC GCTATCTCTC 50
GCTCTCTCTC GCTCTCTCGA GCTCTCGAGA TATAGCCGAG ACACGAGAGC 100
TCGCTCTCTC CCGCGCGAAG ATCTCACCCC CGCGCGCTCG CGCGATATAT 150
30 ATCTCCTCGC GCGCGCGCCG AGCGCGCCCC T 181

(2) INFORMATION FOR SEQ ID :891:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

450

(xi) SEQUENCE DESCRIPTION: SEQ ID :891:

	CTCTTTAATA GCAAGCGAAT GGTAATTACA TGGTCGGATG AGGTCCTCAC	50
5	TCTCAGGGGA GGGAGGAGGG AGCAGAGGTG GACAGGGTGC AGTATAGGAT	100
	TTACACTGTT TGAAGCATCT AACGAAGGGC AACAGTTTTT GGCAACCCAA	150
	TTCACAGTTT TGTAATTTAC AAGAGATTTC TTTGAAAGGA AATAGGAAGG	200
10	CAAAGAA	207

(2) INFORMATION FOR SEQ ID :892:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 198 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :892:

25	CTATCACTTC AGGGAAACAA ACAACTAACA GCCATCAATT CAGAGGGAAG	50
	TGATTTTACA GTAGAGTGAA CGAACTTGG GAAGGAAAAC ATCCAAGAGG	100
	CGTCTGTTTG ACGTGGGTAA CGTGGGGAAC GCATACTGTC TGGCAAGAAT	150
30	TCTACTAGGA CCACGGGAAA CAAAGCAGAT TAAACACTC TCTACTCT	198

(2) INFORMATION FOR SEQ ID :893:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 96 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
40	

451

(xi) SEQUENCE DESCRIPTION: SEQ ID :893:

CTTTAGAGAA TGCCTTGTGG AAAAAAAAAA AAATGGGCCC CAATACTTTT 50
5 TACTGCCCTT TATCAAAATT GTTGTGCATG GACCGGGCCA AATAAG 96

(2) INFORMATION FOR SEQ ID :894:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :894:

AATTGTATAC CAACATATAA ATTAAAAGTG TTATGCAATG AGAAACAATA 50
20 ATGGAAACAG CATAATACTA CATACTATCG CGCGGGGTG TCGGCGTGGT 100
GGGCGTGCGT GTAGAGAGAG AGCAAGGGCG TGTGCGTGAG TGGGCGTAAA 150
25 GAGTGAGCGT GGGAGGGTGT GGTCGGTGGA GGTGTGTGGA GAGGTGAGTG 200
TGCGAGAGGG GCGAGTGAT GTGTGATAAG TATAGCGCGC AAGAGGCGAG 250
GACAAAATAT ATATATATAT AGATATAATA GATATGAGAG AACACTAAAC 300
30 AATAACCACT ACTCACATAG AATAT 325

(2) INFORMATION FOR SEQ ID :895:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

452

(xi) SEQUENCE DESCRIPTION: SEQ ID :895:

ATAGTTGTAC ATTTTATGG GGTGCATGTG ATATTTTGAT ATGTGCATAC 50
 5 AATGTGTAGC AATCAAATCA GGGTAATTGG GATATTCATC ACCTCAAACA 100
 TTTATCATTT ATTTGTGTTG GAAACATTCA AACCTTTTCT TCTAGCTATT 150
 TATCCATTGT TGGATACTTA TATCAATTCT ATATCTTAGC TGTTGTGAAT 200
 10 AGAGCTGCAA TAAATGTAGG AGTGCAGATA TCTCTTTGAT ATACTGATT 250
 TCTTTCTTTT GTTATA 266

(2) INFORMATION FOR SEQ ID :896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :896:

AAGAAGAGTC TTCTGCACAA ACAAACCAT AGTGTGACA AATAGTCATG 50
 GCCAATGGCA ATCTGATGGT CCAGCGGCCC TCGGATGACT CCTCTGCAAG 100
 30 GAGCATCTTC AGGGTTCTAG GGAAGTCACA GGGGCAACAT ATTGGAAACT 150
 AGCAGGCCCA GAAGACCGCC CCGCCCCCA TGCCCTGGCG CAGGGCC 197

(2) INFORMATION FOR SEQ ID :897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :897:

5 GATGGCTGGA GTAGATTAGG GCGTAGGTAG AAGTAGAGGT TAAGGAGGGT 50
GATGGTGGAC TATGATGGTG GGGATGATGA GCGCTATTGT TTTTGTGAA 100
TATTTTCTT CCGACTAACT CGCGCCCCAC TCTCTTGGCA GCACAAACAC 150
10 ACGCGCGCGT GTAAGCGGCG CGAGACACGC GCCCCTTCCC CT 192

(2) INFORMATION FOR SEQ ID :898:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID :898:

25 TGGATGTTTT CATTGCAAA TCATGAGAAA CTTAAGTGGG TTTTATGCAC 50
TTGATAGAGT TGGCAAAATT GAACTATGAA GTTAACTATT TAACTCAAGG 100
AATGGGCGGC AAACCCATCC CCTCGATTGA TAAAGAAGGG GAACATTTTT 150
30 ACATTAGAAC TGACACTGAA AACATAGCTC TTTTTCAGTC CACCCTGGTT 200
GCTCTAGTAG CCCACAGCCC AATC 224

(2) INFORMATION FOR SEQ ID :899:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

454

(xi) SEQUENCE DESCRIPTION: SEQ ID :899:

	GAGGTGATTT CTCAGAGTTT AGAGAATAGG ATGGGGAAAA TTATATTTAG	50
5	TGAGTTATAA CCAGAATTAC ATAAGACAGA TATGGAAATT TTATAAACAA	100
	AATGCAAAAT ATTCTAATGT TTCAATGTTC TACATGAACA TATAGGGAAG	150
	CATAGACAAT AGCCAAAAAT ATGTTCTGCA TTCATATACT AGTTCAAGTC	200
10	CGAGTCTGGC TACTTTCTAG GTAGTGTGCT TTTTGTCAAA TTATAAAGAT	250
	ATATTCCCTT TGTTTTTTGA AAACGAGTGA GATGCTTAAA TAGAGTACAA	300
15	TTATCTCATT CAAAATGTAT GTTGTTTCCT CTCGAGAATT GTGAAGGTTC	350
	TGAGATTGA TT	362

(2) INFORMATION FOR SEQ ID :900:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :900:

30

	GTATGTAGCC CAGTGGGTGT CTTCCACAG GGTAGGTACT CAGTTTGCTC	50
	TGGAGGGTGA CTCATACCTA AACAAGTGCA CATCTCCTTT CTCAGTAAAG	100
35	CCAAAGCAGG TTTCTACATT TGGAACAAAA GAGATCCTGA CCAGAGAGCT	150
	ATCACTGGTG GTCCACTTGG GCCCTCCTTG ATGGGTGTGT TCACTTAGAA	200
	AACCAAATTA CAGATCTGAA GGCTGCTGGG TAGGGACAGG ATTAGAACAA	250
40	AGGGAATGAG ATTGAATGTT ATTTAAGGGA TATTTCTGTC AAGTTTTGGT	300

455

TTCTCGATGA

310

(2) INFORMATION FOR SEQ ID :901:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :901:

15 TTCCCCCATG AGACCGTTAG TCTCTCTTTG CCTGGCTGAC TACCTGCATA 50
CAGTAGGCAC TCACTGCTGG AGTGAGGCAC TGA CTCCTCC AAAGATTGCA 100
GGGGGCGGAG GAGGGAACCA CGAAGGCCTG GGAGGGGGCA TCTTTGGCCC 150
20 CCACTAACCA TCTCCCTATT TCTGCATCCT GGTGA 185

(2) INFORMATION FOR SEQ ID :902:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :902:

35 ACAAGCTGCA AGATCCTTCA CTTGAGGCTT TCAGCCTTAT TCTCCTCCTG 50
TCAAACA ACT AA ACTACTCC GATGTTTGAT GAAAATTAAA CTGCTACTCA 100
GGATACTGCA ATTACAAGGA GAGGGAATGA TCAGCCCAGG GAGGCTATTA 150
40 CGTGTGACCT TTGAGATGGA CCTGATCGCC CCTTTTACTT TTTAGACTAC 200

456

AAGTGCAGGG AGGTGGAGCT TATTTGCATT TGAACCTCTG TAAAGAGTAA 250
GAATATGGAA AGGATGAAGC CTCATTTCATT CGGGCATATT AAAAAGAAAT 300
5 TGCCTTCAGA AACACTTTGC CTTTAAATAT GTGTAGCTAC AGTAAGTACC 350
AATGGGCTAA CTAATTGAAG CTAACATTTT A 381

(2) INFORMATION FOR SEQ ID :903:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :903:

20

CATCAAGGGT TTTTCCTGCT GCAATTCTTG TCAAAACTG ACATATGTAT 50
ATCGTTCTCA ACTGGCAAGC TGTTAGACTG GATAGTCCAT GAATAATAGC 100
25 CTCTGCGCTG TTGCGGGTCC TGC GGAAGTC CTCGGAGCGG CCGTCGCGGA 150
AAGCTCGGCA AAGAGAGAGG CAGAGGAAAT CGAGCATCCA GCCGGCAGCC 200
ACTTTTTTTT TATCGGCACC AGGCCGCGTC CTCCTCCTCC 240

30

(2) INFORMATION FOR SEQ ID :904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :904:

457

	CCCTGGGCAG GCTGCTGGTG GTCTACCCTC GGACCCAGAG GTTCTTTGAG	50
	TCCTTTTGGG GATCTGTCCA CTCCTGATGC TGTTATGGGC AACCCTAAGG	100
5	TGAAGGCCTC ATGGCAAGAA AGTGCTCGGT GGCCTTTAGT GATGGCCTGG	150
	CTCACCTGGA CAACCTCGAA GGGCACCTTT GCCACACTGA GTGAGCTGCA	200
	CTGTGACAAG CTGCACGTGG ATCCTGAGAA CTTCAGGCTC CTGGGCAACG	250
10	TGCTGGTCTG TGTGCTGGCC CATCACTTTG	280

(2) INFORMATION FOR SEQ ID :905:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 225 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :905:

25	GTTCTAGTGG TAACTGCTGC TTCTGGAAAA TATTTAGAGA AACCAACGGT	50
	AAAAAAAAAA ATAATAATTA ATACCGTTGG TTTCTACATA CACTCTCAAT	100
	ATTGTCACGA GTAAAGCGTA GCAAGTTTAA CACAACTTAT GTAAACTTGG	150
30	AAAATTTTCC GAAATTTTAT TGACTTTTCT CGGTCTCTCC TATCTTTATA	200
	TACACATCTC TCATGCACAC ACGCG	225

35 (2) INFORMATION FOR SEQ ID :906:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 161 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

458

(xi) SEQUENCE DESCRIPTION: SEQ ID :906:

5. GGTGCTGACA TCTTCAAGAG CATCTGTCAC TGAATATTGC CGATCTCGCA 50
ACCGGTTCCA GTTAGACAGA ACATTGTGAT ATTCAAACAC TTTCTCGTAA 100
TTTCCAATGG AGTTGTAAAG TTTAATGAGA CCTCGATAAT CATATTCTAG 150
10 TCCACTGTAG C 161

(2) INFORMATION FOR SEQ ID :907:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :907:

AGAGATATAT GCAATCTGGT AGTCCATTAA ATGAGAGTTA CACTTAAAT 50
25 ATTTTAGTTC TTTTAAAGAA AAAGTCTCCA TGTGCTATTT GGGAAAACCT 100
TCATTGCCTA AAGACCCACT TGCATAATTA AGGCAGATGA TGATGATCTT 150
30 TATATATGCG CACACACACA CACACACGAC ACGACGACAC ACACACACAC 200
TCTA 204

(2) INFORMATION FOR SEQ ID :908:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

459

(xi) SEQUENCE DESCRIPTION: SEQ ID :908:

	AGTTTCTGCA TTTGGTCTGT GTGACTCTAT GGAGCCCAGG ACTTACAGAA	50
5	AAAGGTGTAA CTGGCTCTTA GGACTTTAAG CCACATTATG GTAGTAGACC	100
	TGCCGTTTTA TTTGACATGG TGAAATAAAC TACCACTCCT TTGTGGTACC	150
	ATATGGGCAG GACAGAGCTC TTCAACCCTG GCTAACAAGC CTGAAGAAGA	200
10	CCCTGTGAGG CCGCAGCAGC CATGGGAACT TCCCAAAGGA CAGAAATCCA	250
	CATTGGAACG TAGCATCCAG ATAGGTGACA GAAATTCCTT CCACCATATC	300
15	CAAATGTGTG TGT TTT	316

(2) INFORMATION FOR SEQ ID :909:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 307 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :909:

	CTAGTAACAT AGAAAATAAA CTTCAGTGGG AATCTCTGCT TCCCGCGTGA	50
30	GGTGT TTAAT TCTTGGCATT TTTGTATTTT AAAGATGTAG CAACTTGTTT	100
	CAAGTTAGAG GAGATGGCAG GGTCAAAATT TTAGAACTG GATCCCACCA	150
35	CCACTGTGTT ACTTCCTAAA CCTGCATACA AATGTTCTGC CAACATGTAA	200
	TGTGCCAATA GAATTATACG GTGTGAACTG CATATCTCAG TATCTCCACG	250
	GGAAAAAACT GTGGTTGGGG CATGGAGGGG GGAAAGGGAA ACTTTTTTAA	300
40	GCTATTT	307

460

(2) INFORMATION FOR SEQ ID :910:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :910:

TTTTTTTTTT TTTCCAGGCA CCTAACGATT TGTTTGCTC AATCAAACGC 50
15 AGACAGGCGT CTCCGAAGTA CCACCACTGG GATATCCTCG GACCAGCGCT 100
TAAACCGAAT CCCCAACAATC TCAAACCTCAA CCAGGCCAAA GGAACACAG 150
TGACACAACA ACAGGGTTCC AA 172

20

(2) INFORMATION FOR SEQ ID :911:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :911:

GCATAGAGAG ATATATACAC AGAGAGGACA TACATATATA TATATAGAGA 50
35 CACAGAGACA GACATATAGA GATATATATA TACACAGCAT AGAGATACAG 100
AGAGATAGAG AGAGATACAC ATACACACAT TCATCAACGA GAGAGAAGAG 150
AGGAAAGAGA GAGAGAGCGA GCACAGACAG AGATAGAGCA CACAGAGAGA 200
40 TCGCGCAGAT CTATACAGAG GGATATTCAC CACATTGTAT ATGGAAAGCG 250

461

CATCT

255

(2) INFORMATION FOR SEQ ID :912:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :912:

15 CAAGCGAATG GTAATTACAT GGTCCGATGA GGTCTCACT CTCAGGGGAG 50
GGAGGAGGGA GCAGAGGTGG ACAGGGCGCA GTATAGGATT TACACTGTTT 100
GAAGCATCTA ACGAAGGGCA ACAGTTTTTG GCAACCCAAT TCACAGTTTT 150
20 GCAATTTACA AGAGATTCTT TTGAAAGAAA ATAGGAAGGC AAAGAA 196

(2) INFORMATION FOR SEQ ID :913:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :913:

35 ACTATCACTT AAGGGAAACA AACAACTAAC AGCCATCAAT CCAGAGGAAA 50
GCGATTTTAC AGTAGAGTGA ACGAACTNG AGAAGGAAAA CATCCAAGAG 100
GCATCTGTTT GACGCGAGCA ACGCAAGGAA CACATACCGT CTGGCAAGAA 150
40 TCCCACTAGG GCCACGAGAA ACAAAGCAAA TTAAACATT ATCCACTACA 200

462

CGA

203

(2) INFORMATION FOR SEQ ID :914:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :914:

15 CTGCCGAGCC ACCATGCTTG CCTGAAGCTT CGGCCGCGCC ACCCGGGCAA 50
GGGTCCTCTT TTCCTGGCAG CTGCTGTGGG TGGGGCCCAG ACACCAGCCT 100
AGCCTGGCTC TGCCCCGCAG AACGGTCTGT GTGCTGTTG AAAATAAATC 150
20 TTAGTGTTCA AAACAAAATG AAACAAAAAA AAAATGATAA AAAAATCGGA 200
TTTCCGGTTA ACACTGTGAC TTCAATTGAA ACACCTTTTT GTAGTATCTG 250
25 GAGGTGGACA TT 262

(2) INFORMATION FOR SEQ ID :915:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :915:

40 TGGGTTCTAA TGATGTGCTT GAAGAGGAAG ATTTTGATCG CACCACTGAT 50
ACACGGAGTC TGTATTTTGC ATCCTAGAAT GATTAACCAG AAACAAAGAA 100

463

AGGAAAAAGG TAAATCAAT AATAAGATCA GCAGCTCTGG GACACAGAAT 150

AAAGAATGAA ATAATTGAA AAAAAAGGCA GGGCAGGCAA A 191

5 (2) INFORMATION FOR SEQ ID :916:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :916:

AGACTTGGGG GTTCCTGGTG TGTGAGGGGT CCTGGGATAG CTAGGGGTTT 50
TCCAGGAGTT GTCCTTTGTT GTTTGTCGTG AAGAATTATA CTTTGTGTGT 100
20 GTGTGGGTTG TCCCATGTGT ATGCGTGTAG TGTGACAGTA TATGACCCCC 150
AGTGTGTGCA TATGTTTGTG TGGTTGTCTC TGAGTGATAT CCACCTCTCT 200
25 CTCCCCCTCT GTCTCTCTGC AGAGATATGT GTGGCGTCAC TGTACTCTTG 250
TG 252

(2) INFORMATION FOR SEQ ID :917:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :917:

TAGACAGAGT GACAGTGAGA GAAAAAGAGA GGAAGGAAAA GGGAAAAGGA 50

464

GTAGGGAAGG ATGAGGGAGA TAGGAAAGCA CCTAC GAG GCAGAGAGTT 100
TCCTGAAGGT CATGCGATCC TTTACCCTCA GAAACTTTCA GGCTGAAATC 150
5 ACCATCTCCG TTATCCCAAC AAACGCACTC TCCTACCTCT ACAAGCACTT 200
CAAGTAAAGC AGAAATCACA CCAATACTGA CGNGCTTCAA GCGCAAC 247

(2) INFORMATION FOR SEQ ID :918:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :918:

20

ATTTGGATTC AATTGCCTGT TGCACCTTTA CATTAAGTGT TGCTTAAATA 50
AACAAAAATA GAGCATAAAT TCAATATTCT ACTGTCTAAA CATTTTAAAG 100
25 CAATGGTTAT GCCATCATAA ACAAGTAAAA TGCACCTAAT TCGAGTCTTT 150
TGACACCTCT TGTTTTAAGT TTCCTGTATG ATAAAGTTCT T 191

(2) INFORMATION FOR SEQ ID :919:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :919:

40

CAAGAGTGAG ACTCCATCTC AACCAAAAAA AAAAAGAAAG AAAAAAAGAA 50

465

ACAACCTCCT CATTTTCAGA AGCGAACACA CCCCCGCCCC AAGATAGACG 100
ACAGAGACCG GACTAAGATT TAACCCAGGA ACTTTTCGCT TGGGCACCTT 150
5 CGAACAACAC ACAACCCGCA AAACCATACA CGCTCCCTTG CCCGAGGCCC 200
AACCC 205

(2) INFORMATION FOR SEQ ID :920:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :920:

20

GACAAAATTG GGACTCTAAG TATTGCGCTT TTTTTCCTC TCCAACGACT 50
CGTTCCCTTT CAACAAATAG CACTTCAGTC CACTGTGTAC AGAAGTAATA 100
25 CATCTCCTAT CGTTAGTTGA ATAAATTCAC ACACCGCGTT TAAGAGATGA 150
AACCACGACT TCGTCAAGCC ACATTCGATT GCCATAAGAT TCCAAAGAAT 200
TCTATCCTCT TAAAGCGAAC CACATGTAAC CCGAAGGTCC CCACCTATCA 250
30 AGGTTAGAAC TGATATTCAA ATTATAGACT CATTCCACTA AGCAAGTAAG 300
CTCTAAGCTA CAGGTTGATC ATA 323

35

(2) INFORMATION FOR SEQ ID :921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

466

(xi) SEQUENCE DESCRIPTION: SEQ ID :921:

5 AACATTGACG ACGCTAAGGA TGCCATGATG CCATGAATGG GAAGTCTGCA 50
GATGGACGGC AGATCCGAGT AGACCAGGCA GGCAAGTCGT CAGACAACCG 100
ATCCCGTGGG TACCGTGGCG ACTCTGCTGG GGGTCGGGGC TTCTTCCGTG 150
10 GGGACCGAGG CCACGGCCGT GGACTCTCTA GAGGCGGCGG GGATCAAAAC 200
TATAGAAACA ACAAGTTAGA GTACAGACGT 230

(2) INFORMATION FOR SEQ ID :922:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :922:

25

TATTTTTCCT GATGTTCTCC CTCCTCCAG TCCCCGACCT CCCACAGGCC 50
CCAGTGTGTG TTGTTCCCGT TCCTCGTGTC CGTGAGTTCT CATTGTTTCT 100
30 TGCCCATTCCT GAGGGAAAAC ATGCCAGTGC TTTCGCGTTC TTCCTCGCTC 150
TCACCCACCT CTCAGCTTAT CGCGTCGCGC GCGCAGTATA TTCGTCTCTC 200
TCTCCAGTCT CTCTCGCGAC ACACATCTCT CTTTGTAA 239

35

(2) INFORMATION FOR SEQ ID :923:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

467

(xi) SEQUENCE DESCRIPTION: SEQ ID :923:

5	GTCAGTTCAG TTGTGAACAA AGCCCTTTGT GTACGTTTTT AAATTTTAGT	50
	TCACACGATA ACAATGCTTT GCAAGTAGGT GTAATTATTT TACTCCCATT	100
	TTATGGATGA GAAAACAACA GAGAGGTGA TTGGCCCCAC CTTCAAATCC	150
10	TGAAACCCGT CCACTCAATA AATTTTGT	178

(2) INFORMATION FOR SEQ ID :924:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 325 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :924:

25	CAGCTGGTCC CCCACTAAAA GAAGGGGCAG ACCACCACTA GCCAAAAGAG	50
	ATAGCAAGAC TAACATCTGG AAGAAGCGAG AGGAACGCCC ACTGATTCCC	100
	AAAAAAAAAC TCCAATGGGG ATTGTGTGTC TGCTGTCTCG TGCTGTTTAT	150
30	TCTTGCTTCT TGTGTAAAT TGCAGTACGA ACTTAAGAAA ATGAGACTGA	200
	GCAATCTCAT GGTTCCTTGA CATGTCTCAA GCAGAGTAAA TGGTAATTCA	250
35	GTAATCAGAG AGAAAGATAC CAAGGAATGC TTTTCTGGC CTATTCATTT	300
	ATTTTGGGG GATGAATTTA CAGTA	325

(2) INFORMATION FOR SEQ ID :925:

40

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 261 base pairs

468

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :925:

ATGGCTATGA CCTGGGACAT GGAAACAGTG ACCTCCGCGT TCTGGTCCCG 50
AGATCCTCGC ATCAGCGTCA TCGTGTGCAC CGCCTTGGGG GGCTGGAGTT 100
CCGGTTTTCT TTGTTTTTTC TCTTTATTCTG TCCTTTCTCA AAGATGGGAT 150
ACTGATCAGA ATCGTTCTGT ATATGCTTGG GACTGGATGG AAAGACTTTG 200
AAGCAGCTGT GGGGGGCGGG AGGACACCGA CAACCAAACA GACGTGTTGG 250
TTCCAGTCCT G 261

20

(2) INFORMATION FOR SEQ ID :926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :926:

GTCAGCCTGG GCAATCACAA CGACAACAAA AGGTACAGTC TCAAGAGTCC 50
AACTGGGTTC AAATCCTGGC TCTGTACAT ACTAGCTGTG TGACCTTGGC 100
CAAGTTTCTT AACCTCTCTG TGTGTATAGT CCTTATCTGA AAATGGGGAT 150
AACCAACCAA GAGAGCTGAG AGA 173

40

(2) INFORMATION FOR SEQ ID :927:

469

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :927:

10

AACACTCAGA CCGGACGGGA CGAGGGATTC CCCTGCCTTC GCTTCCCTCC 50
CTCGCTTGCT TTGTAGTTTT CCCGCACCAG CCCGCTGCCC TCGCCCATCC 100
TAGGGCCTCG AAGCCCGGGG AATCTGTCCC ATCCTGTAAC GGGCCGCCCC 150
CTTNGATTTT TCTGCCCCGTG CCACCGGAGG TTGCTGCGAC GCGCACCGAC 200
TCAGATCATT ACTACTGAAC TCG 223

20

(2) INFORMATION FOR SEQ ID :928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :928:

GTTATAATTA TTTACATGCT GCAACACGTC ACAACATAAA TTTACCAAAT 50
ATTTTCATGGT GGGATGCTGT AGGTTTCAGA TAATAGTTTT AAGATAAAAA 100
CCACAGATTA AGTGAAGACA CCCACAACCT TAATGACTCT ACGACTCTCG 150
GTTGCTAAAT GCTAGAAGTC AAAAGGCAGT GTTTTTTCAG TCCTACCTGT 200
CATAACTTGC AT 212

40

470

(2) INFORMATION FOR SEQ ID :929:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :929:

TTAACATAAT ATTTTGAATA TATAGGGCTC ATAAGATATA TTATTAAATT 50
15 ATAAACAAAA TAATCAGGAA CTTAGTGTGG TGCCTAGTTT GATATATGAT 100
TACTTTTTGA AATGCACTAA ATTCCACAAA TAATGAAAGT ATTCTTTGTG 150
TATAATGTTA TGTGTGGTTA TTATGTATGG TCTTCGTATC CAAAGGTATG 200
20 ACATAACTTG AGTTTGTGTTG CTGGTATTT ATT 233

(2) INFORMATION FOR SEQ ID :930:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :930:

35 AGTCTGTAAC GATACACCCA TAGATGTGAA TTATGTATAT TCGAGAAGGA 50
GATCAGATGG CATCCAGAAG ATAGTTTAGA TTTCAGCACA TTCATGGTTC 100
AGATGCAAAA TCAGATCATC AAATAGATCC AGCAATTCAC AATCATCATA 150
40 GCCATATCGC GTCACGTCCG CCGCACAAAG ATCCGCACCA ATTATCTATC 200

471

TCCCACCCCC CCCAGGCATT CAGCACCCGC AAAAG

235

(2) INFORMATION FOR SEQ ID :931:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :931:

15

CTATCTAGAA TTAATTATTT CACTTGAAAT GTATGGTTTC AGGAAAATTT 50

TCAATTTAAC TTGAAGGGAT TATCTCTTAT TTTGCTTGA ATAATGGCAT 100

CTCAGAAACA TGGGTTTACC TGTGATTTTT TTGTTTGGGT GAATGCTTAA 150

20

AAACAAAAAA AAAATTTACA TATGCATTTT ATGGATACAC ACACACACAC 200

ACACACACAC ACAAAAAACA C 221

25

(2) INFORMATION FOR SEQ ID :932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :932:

TGCTCTATTG CTATCTCCTG ATATAGGTTA TATATATATT ATGTCTTGAG 50

CGTCATGTCT TGTGCTACTA CACCGTGTTA ATCCCAGCTA CTCAGGAGGC 100

40

TGGAGGATCG CTTGAGCCCA GGAGTTCTGG GCTGTAGTGC GCTATGCCGA 150

472

TCGGGTGTCC GCACTAAGTT CGGCATCAAT ATGGTGACCT CCCGGGAGCG 200
 GGGGACCACC AGGTCTGCCT AAGGAGGGGG TGAACCGGCC CAGGTCGGAA 250
 5 ACGGAGCAGG TCAAACTCC CGTGCTGATC ATGTAGTGGG ATCGCAGCCT 300
 GTGAATTAGC CACTGCACTC CAGCCCTGAG CAA 333

(2) INFORMATION FOR SEQ ID :933:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :933:

20

AGATTTATGG CTGCTTTCAC TTGGCTCCAT GTTCTGCTGA TAATTAAACA 50
 GTTGTGTGT CCTGTCTTTC CTCAAAGGAA CTTGTCAACC TTTGGAATTT 100
 25 GTTCATCTC AGAGGGACGT CTTAAGTACT CAGCTTTCTG AATGTTTAAG 150
 AAAAAAATAA TACTTTTCAG AATTACCTAC CTCTTTCTCA TTTTTCAGCT 200
 GGGATCAATT ATCCCTTTC AACTTTTTTT ACATCCTAAG TAGAAATAAA 250
 30 ACTCTTTATT CTATTTTTTT TCAGTTATTG G 281

(2) INFORMATION FOR SEQ ID :934:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

473

(xi) SEQUENCE DESCRIPTION: SEQ ID :934:

5 AATCTTGTAT TATGTTAATA TTAAATCTA ATAATAAGAT ACTGTAGAAG 50
TATTTTACAT TTTTGGGGTA TAGGCACAAA TATATACATT TAAATATTAG 100
TAATAGAATT GAACAATTAA CTATAAATA TTATATCATA ATAACTGTT 150
GTTTTATCCC AAGGGTAGAG GGACTCTAAG TAAACTGTA ACAGAATCAA 200
10 AAGGTTACTG ATAGTTAGAA TGGGTTGAGA ACTATTTTAA CTTGGGAAC 250
TTAAATAAGT AAATCT 266

15 (2) INFORMATION FOR SEQ ID :935:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :935:

GGAAAACAAA TGTAAGGAGG GAATTCAAAT ACCTAGTTAA TCTATTAAC 50
ACTAATAACT CATTAAATAA ATTAATAATA TTAAATGATC TGTGTGTTCC 100
30 ATGCAAATAA CAGAATGATT TCCACTGAAT AGTCATGATG GTTTAAATA 150
TTACTCTAAC ACCAATAACA ACACGTAA 178

35 (2) INFORMATION FOR SEQ ID :936:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

474

(xi) SEQUENCE DESCRIPTION: SEQ ID :936:

5 ACTCAGCTCC GTGCGACCCA CATGGCCCCA GGCGGGGGGA CACCAGAGGC 50
TCCTCCATGA GCAGCAGGAG TGAGCGGAGG AATGTGCCCC ACAGCAACTT 100
TCCCAGCCAA TGCCACGATG GAGATGACAA CCCCAGATCT GGGGANACAG 150
10 AAACCACTCA GAACGGCACA GGGTAACTGG CCCCAAACGC TGAAAGTTAG 200
ACTTCACCCG AATTACATTT ACCA 224

(2) INFORMATION FOR SEQ ID :937:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :937:

25

ATTTTTTTTTC CCAAGAATCC CCAACTCAAT AAAACCGTGA AACAATTGCT 50
GGGGATGGGT AGAGAAAACC CATTATAGT ACTTTTCTGC CTTCTTGTGG 100
30 TTTTCGGCTT TGCGATCAGG GACTGAAGAT AGAAGGAAAA AAAAAAAAAA 150
AAAACAAACA CAAAAACATT TCAAAAGAGA AAGGAAAAAA CTTTTTCCAA 200
CCAAAACCTCC TAAAAAACCC AAAACAGAA CAACCAATTA AACCCGACCC 250
35 GACACAATA CCAATGACTG 270

(2) INFORMATION FOR SEQ ID :938:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid

475

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :938:

	AGCCTTCTCC CTATTCGATA AAGATGGCGA TGGCACCATC ACAACAAAGG	50
10	AACTTGGAAC TGTCATGAGG TCACTGGGTC AGAACCCAAC AGAAGCTGAA	100
	TTGCAGGATA TGATCAATGA AGTGAATGCT GACGACAATG GCACCATTGA	150
	CTTCCACAAA TCTTCAACTA TGATGCCTAG AAAAAAGAAA GATACAGATA	200
15	CTAGAACTAA AGTCA	215

(2) INFORMATION FOR SEQ ID :939:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :939:

30	TGTCGTCCTT AATATTTCTN AGCCTTTTGT CATAGAGGTG GTCGGTTGGA	50
	CCTCAAAGCC TCCATCTAAT TTTTTTTGTC TATGTTTCTA TATCTCTCTC	100
	TTTTACGCTT CTTTCCCGGA CCGTCCCCTC CCTCTACAAT TATATTTACT	150
35	ACCTTCATGA TTGCTTTTTA TTATTCTTT CACTCATCAT TATTGTTTAT	200
	TTTTTAATTA ACAATTTTTT TCATTATTCT TTTTCTTAAT TTGTAACCCG	250
40	TTTCTAATTT TCTCAATTAT TCGGCTTTCT CAACCCCCCT CCTTCCTCAT	300
	TAC	303

476

(2) INFORMATION FOR SEQ ID :940:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :940:

ACACTATTTT CAAAAATCCA AATAAAAGTG CAGTTTCAGA CTTTTTAAAA 50
15 AAACACCGTT GACCTGTCTT AGTTGTACAT TCAGAAAATG TAGCCTCGAG 100
CGTTTGCATG CAACACTGCA TATTTTTTCT AATCAGATTA ATATGAGTTT 150
TAATGTTTAG CATGAACTAC AGCTAAGGAT AAAAATTTTA AAGTAGCTTT 200
20 CATAGTCTAG ATTCCTGGTT TCATAATGCT TTATGTAGTA CATTTCAGTT 250
TGCTTTGCTT TGTGGAGACT TCGCGGTATT TTCTTTTGCT TGTGTGTTTA 300
25 TCGCCAGGCA GCGCTGTTCG AACTGTGAGA 330

(2) INFORMATION FOR SEQ ID :941:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :941:

TTTATTTCAG ATAATTTTAT GTAAACAAAT TAAGAGTTAT TCATTCAAAT 50
40 TTTTGGCAGT GTTAATCTGT AAATGATGAC TTGATGTACA GAAAATGCAT 100

477

TTTTGCT

107

(2) INFORMATION FOR SEQ ID :942:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :942:

15 CCACAGCATA CACACCTTGG AAACCAAGAA GACTCTTTGT GTGTGTATGT 50
GTGCGAGACT GACGCGTCTC TACGCGCTCT ATGGGGGGAG ATTTGGTTAT 100
TTCGGCGTTA CACCTCCGGT GTTCTC 126

20

(2) INFORMATION FOR SEQ ID :943:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :943:

ACTGAACAGC CGCTGGTTCC AGAACAGGCA CAGAAGGCTC CAGCGCTAGA 50
35 AACAACTGGC ACAGGAATGG TAACAATAGT CTGGCTCAGC CACAACAGGA 100
GGCTCCGGGA CAGTCACAAC CGAGAGCTTC CAGGACAGTT ACAGTCTGTA 150
AGCTC 155

40

(2) INFORMATION FOR SEQ ID :944:

478

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :944:

10

CGTGAGGAGC AGGTACCATT TTTAGTAGTC ACACAATTCC ACCTCCTGTT 50
TTTACTACTG GCAACTTCTA CTTGAGAATA ATGTTCTGAA AATGGAGGTG 100
GGGGGGGGTT TGGAAGCAAA CACATTTGGG GTTTTAAACC AATTGTTAGG 150
TTCTTTTAT TTAGGGTTGT GCAGGGAAC GTTGGGAGGT TTCTTTAGGT 200
GGGATGGGGG GACTGGGTGT TGGTTTTTGG GGGGTTTTTG GGACGGGTTT 250
TATTTTGTCC CTTAACTGG TTTGTTGGGC AGGTGGG 287

20

(2) INFORMATION FOR SEQ ID :945:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :945:

35

ATCATTGATC AATGATATGG TTTGGATTAC TGCCCCGCCC AAATCTCTTG 50
TCCAATTATA ATCCCCAGCA TTGGAGGAGG GGCCCCGTGG GAGGTGATTG 100
GATCATGGGC ATGGACTTCC CCCTTGCTGT TTTCGTGATA ATGAATTCT 149

40

(2) INFORMATION FOR SEQ ID :946:

479

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :946:

10

TTTAAACTGC AAATAGTCGT TACAAAAAGT TTTNNNNNTT CTTTAAATA 50

AATTTCACAC AAAGAAAGAG AAATAGAAAG CGACGGTACT GACCAGCAAG 100

15

AGGAATAATA ATTACATTCA TCTTAATGTG TGTGTGCCAG TTCTGTTTAC 150

ATTAACATTG GAAACTCCA GACCTGGACA CCAGAACCTC AAATCTGTGA 200

GTGGAATGTC TTGAGATGGG CACGCTGGAA GTCAAAGGGT TTCTCTTTT 250

20

TTTTTTTCCC C 261

(2) INFORMATION FOR SEQ ID :947:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :947:

35

CTTTAGGAAC TGTCAGCATG TTGTTGTTGA AGTGTGGAGT TGTAACCTG 50

CGTGGACTAT GGACAGTCAA CAATATGTAC TTAAAGTTG CACTATTGCA 100

AAACGGGTGT ATTATCCAGG TACTCGTACA CTATTTTTTT GTACTGCTGG 150

40

TCCTGTACCA GAAACATTTT CTTTATTGT TACTTGCTTT TTACACTTTG 200

480

TTTAGCCACT TAAAATCTGC TTATGGCACA ATTTGCCTCA AAATCCATTC 250

CAAGTTGTAT ATTT 264

5 (2) INFORMATION FOR SEQ ID :948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :948:

CCTCGACTTA CCACGGGTGA TCCCAGAATG GACTATCAGC GGTGTTTTGA 50

GCCAGGTTGA TTGAGCACTG GGCTCCAACT TATTGTTAAT GAGAAACGGC 100

20 CCAACTTGGA CCATGACTTT CCCATTGCA GGTCTTAGAA TAATTTTTT 149

(2) INFORMATION FOR SEQ ID :949:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :949:

35 CGCTCAGGGT GGAAGTGGCC GGGCGCGTCG AATGTGCCGA GCTGGTGCGA 50

GTGGGCGAGC AGAGCGCCTT GAGGGTTGAG CATCTTCTGG ATCCAGCAGA 100

GGCCTCCCAG GAGGGGAGCC AGGTGGCTGA AGGCAAGCAC TTTNNNNAGG 150

40 TTCTAGTCCC CTTTTTAGAT CCTAGGGGAC TGGAGATTG GCACCTTCCC 200

481

CCAAGGCTTG GCCTCGTGCC CTATAGGGTG CCCCCCTCTC TT

242

(2) INFORMATION FOR SEQ ID :950:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :950:

15 ACTCTGCCTG CACTATAAAA TGAACCAAGG AGGATCCAGT TTGCTGTCTG 50
CACTGACAGA TTTACAGACA GGAAAACAAA GCCTTACTTA CCAGGAATCC 100
AAAGTTTATA CATGAAAATT TAAAAGGGA GTCTATGCAA AGCGGAGTTC 150
20 AGG 153

(2) INFORMATION FOR SEQ ID :951:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :951:

35 TGCGGGAGTC TCACTGGGGG GGGGACACCT GTGCAAACGC GTAACGCAGG 50
TTGTTCTTAA GGCGAGCTCA GGGAGGATAC AGAAACTCT CCTGTGGTGC 100
TATGAAATGT GCGGTAAAAA GCATTCTG 128

40

(2) INFORMATION FOR SEQ ID :952:

482

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :952:

10

GTTGGAATT TCCCTAAAT CACCTACCGA TTACCCTTGA TTTCCCTTTG 50

TTTTCAGTTT CTCAAAACGA ATGAAATAGA ATATAGCAGA ATGTTAACCC 100

15

ATATAAAAAT AAAGTGACC CAAATATTGT AATGTATATT GCTGCTCTTC 150

TTCAAATTAA ATAAGGGTTT AAAACCACTT AATTGGTAAT ACAACATCTC 200

AATTGATACA AAT 213

20

(2) INFORMATION FOR SEQ ID :953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :953:

GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC 50

35

TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT 100

TCATTATTTT TTTTCTCTAC CATCATGTAG GCATACTCAG TGTAGACTAC 150

CACAATCCTG GATACCTCTC TGCTTAGATT TACAATCTCT GCTAAGATTT 200

40

GCCACTGCAG AAAGTGTAGT ATTTTCACTA CATTAT 236

483

(2) INFORMATION FOR SEQ ID :954:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :954:

GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC 50
15 TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT 100
TCATTTTTTT TTTCTCTACC ATCATGTGAG GCATACCCAG TGTAGACAAC 150
CACAATCCTG GAAACCTCTC TGCTTAGATT TACAATCTCT GCAAAGATTT 200
20 GCCACTGCAG AAAGTGT 217

(2) INFORMATION FOR SEQ ID :955:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :955:

35 AGCAGCGACC GCGCTCACTG GCTTTTGTGTT TCTGCTTGGG CCTTTTCTGT 50
TCAGTCCATG CTTGAACTAC TCCACCCCTT TAAATCCAAC GTAAAAACCA 100
GTCTTTTCTG TGCTTGTCTT CTGTGCGTTA ATGCTTTTTC TTATGCTTGC 150
40 TTATTGAAAT ACTGTATTTT CATTGTCCCC TGGCCAAAAC ATCTGAGTCG 200

484

TGAAACCATT TTAGATACTC TACTTTCTTA CTGTGTTACG TGGCATTTTA 250
TGCTTG 256

5 (2) INFORMATION FOR SEQ ID :956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :956:

CAAGCAATTG AGAGACTTTT TTCCTGTTAT TTTTCTACCA TTTATTTCTC 50
ATTCATTAT ATTATGGTCA GAGAATATAT TTTGAATGAT TTCATTTATT 100
20 AATTTTAAA AATAACATTA AAAAATTTT TAAAATGTGA ATATACCACA 150
ATACAGTATA AAGATTGTAC ATTCTGTTTT TGGACAGTTT TCTA 194

25 (2) INFORMATION FOR SEQ ID :957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :957:

ATCTATTTTT CTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA 50
ATAACCTAAA AAAACATGTT TTCTCCACAC TAATTTTAGG GTGAATTCCT 100
40 CATTTGCTT TTCAGATCAT GGGGTGAGGG GGATGGTTCG TGTGTGTGAG 150

485

GAACTGAGGA ATCAGATGGA AAACAATGCC TCTGCTCCTT TGAGTA

196

(2) INFORMATION FOR SEQ ID :958:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :958:

15 GCGCTCAGCT GGAACTTCCG ATCTATTTTT TCTTGGTCTC ATACTCAGTT 50
TTTTTATGTA GTCACCTAGT AAAATAAACC TAAAAAATAA CATTGATTTT 100
TTCTG 105

20

(2) INFORMATION FOR SEQ ID :959:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :959:

GACAGCGACC GAACTCAAT GGAATCCCGA TTCCATGGAA ATGGAAAATA 50
35 GCTCTATTTA TACAGCAAAT TCAAATACAG TAGCTTGCTA AGCAACTTCA 100
TAATTCATTA AACTCGATG GCAGAGCAGA TAGTCACAAT TACTAACGAT 150
TATCATGATC TGCATTCTTG ACAAGTATAC TATGGCGAGA TAAATCAAAC 200
40 TCAGACGATG ATAAGCAAAC TCAAAAATGA AAATGATGAT GCCAACTAAG 250

486

CTTTTGTTAA A

261

(2) INFORMATION FOR SEQ ID :960:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :960:

15 CACAGTTTGT TTGACTAAAC TCTACAGAAG TCAGGTATTG GGAAGGAGAA 50
TCGTTTCTTC TTTAGAGGAG TAGGTTTAA CCATGTTAAA TTTCCAAGAA 100
TAAATTTATT TATCACCTCT ACACAGCGCA GACCATTCA GGAAAATAAA 150
20 TAATTTTCGA TTCAAGTACT ATACAACTT AACGATGG 188

(2) INFORMATION FOR SEQ ID :961:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :961:

35 ACTTTCGCCT ACCCGGAGAG GCCCAGAAAA TTGACCAGAT GATGGAGGCC 50
TTCACCCAGC AATACTGCCT ATGCAACCCT GGAGCTTTTC AATCCACAGA 100
CACACGCTAT GCACTGTCCT TCGCCATCAT AACGCTCAAC ACCAATTCT 150
40 ACAACCAAAA AGCCAGAGAC AAACCTGACC TAAAGCGCTC C 191

487

(2) INFORMATION FOR SEQ ID :962:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :962:

CCAAGGCAGA GTTTATTAGG TTTATGCTTT ATATTTATAT ATAAGGTTTT 50

15

ATTCATGTTA AAAACTTAAA ACCAACGGAT TATGCAAAGT GATAAGTGTA 100

TCAATGAATA TACAACTGAC TGGATTTTAA ATATACACAA ACCAGTATAC 150

CCCCAGTACT TAAATGAAGG CACTCAGTAT ACACCAAAT T 191

20

(2) INFORMATION FOR SEQ ID :963:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :963:

AGCAGGCCAA AAGCCCAGGT GAGGCCACGC AGGAACAGCA GCCCAATGCC 50

35

TCCTAGCACT CAAGATCCAC CATAGTCCAA GCAACTGCAG TTCACTTGA 100

GTACAAATAC GCTCCCGACA GCCTCATGCA GCGACACCCT AAAGGACACC 150

CGAACACCAT CAATAACCGA ATAGACTA 178

40

(2) INFORMATION FOR SEQ ID :964:

488

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :964:

10

ACTTTGCAGT CCTCACATCA CAAATAGAGT AAAAGATTCC CAAAAGGAAG 50

GGGATCCTTT TGACTGCCAG ACGCGGGAAG GAAAGAATGA AATTAAAGAA 100

15

TATCCTTTTA AACACACACC TCGACACAAT TTTCCACTCT GCTAAGGGAT 150

CACAAAGACT AAGACGCGGG CAGACTCCCC ATAAGCCACG CTTATAACC 199

(2) INFORMATION FOR SEQ ID :965:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :965:

30

ATGGAGCAGG ACCTGCGATG TTCTGATGGA TTATACCCAC AGTGTATTTT 50

GGCACATCTG CCAAAGCTA CAAACAACCC CTAATAATTA CACACTACAG 100

35

ATAGTGAGAA GCGTCCTACC CAGGAGTCCT GAATGTGATC TGAGTATGCT 150

CTAAGGCAGC CCCAGGAAAA GCAATCCAAT CCCTTCTCC TCGCCTTTAA 200

ACCTGCAGGT TGGGGCT 217

40

(2) INFORMATION FOR SEQ ID :966:

489

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :966:

10

ATTGCGACC AAAATCATCT GGGTTTATAT TTGAAAAAC CTTGTTTTC 50

AATTAAAAA TGCCAAGAAA GTTGTGAATA CCGTTCATTA TCACTAGGAT 100

15

CAAGAAAAAG CAAATGGTTT AAGTTTTTAC ATAGGAAATC TAAGAACTAC 150

TCATCAATAA AACGCAACAC TATCA 175

(2) INFORMATION FOR SEQ ID :967:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :967:

30

AGGGGTTTCAG GCCTGGAGTC AGGGAAGAAG GGGAAAGGGG CAGATAGCTG 50

GGGGACAAGG AAAACCTGGC GCCCCCACC GCGAAAAACA CA 92

35

(2) INFORMATION FOR SEQ ID :968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :968:

	GTAAATATTAG GGACATGAAT GTTAGTACAG TAATTACCAC ACATGGAAAA	50
5	TATTGTTCAG CAGGAAAAGT AAAACTTTCA AAAAATTCCC TAAAGATCCT	100
	ATTCAATAAA CAATTTTAGA TTTAAGGAAC CACTTACGCA AAACTCGAAC	150
10	AAATAACCGA AAACTCCACC TACCGCGCAA TACTCAAAAA CACAAAAATA	200
	CTACTAAC	208

(2) INFORMATION FOR SEQ ID :969:

15

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :969:

25

	AGTGGTTGGT GTTTACTGGA ATCTTGTTTT TTTTTTTTCG GTTTTTTTGA	50
	CTACTCGGGG GGTTCCTT TTTACAGGA ACTAAATCAA CAAACTTTTT	100
30	CGATTCTCA ACTTTAGATT TTTATTTTTT TTGATTACCA TTTACTTTTC	150
	TTCATTTAAA ACTTTTAACG CCTCAGCCTT TTTCTTAGGC CAAGGCCTTC	200
	CACCAAGGAT TTA CTCCGGG ACGGATCTAA CTGGATTTTC CGAGGTGGGT	250
35	TTAAGA	256

(2) INFORMATION FOR SEQ ID :970:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid

491

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :970:

	AATCTATTTT CCTTGGTCTC ATACTAAGTT TTTTATGTAG TCACTTAGTA	50
10	AATAACCTAA CCCGCTTGTT TTTCCACAC TAATACTAGG GCGAATTCCT	100
	CATTTTATTT TTAAGATCAT GGGGCGAGGG AGATGATCGC GAGCACGAGG	150
	ACCTAAGACA TCAGATGAAA AACAAATGCCT CTATTCCTTC AAGTATAATA	200
15	AATGATACCC GAGAGTAAAG AGCTACACTT CGCACCTCTA	240

(2) INFORMATION FOR SEQ ID :971:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :971:

30	ATCTATTTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA	50
	ATAACCTAAT CCGCTTGTTT TCTCCACACT AATCCGAGGG TGAATTCCTA	100
	ATCTAGCTTT TCAGATCATG GGACGAGGGA AATGACCGCG TCGCGGAGGC	150
35	CCTAAGGAAT AACATAGAAA ACACCGCCTC TGCT	184

(2) INFORMATION FOR SEQ ID :972:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid

492

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :972:

	GTGTTCTCTA AGGTGATACC TTTTAATTTT GAAAGACTAA ATAATTTTAA	50
10	TCGAGAATTT CCAGTCTTTC AGTCTGATCT ATTTAATTCA CTA CTGTTA	100
	CATAATCCAG TGAAACTCT ACTTGTGAA ATTATGACAT AAAGATCTTG	150
	CAGCTTTATT TGAGTATTG TTCTTTTGTG TAGTTTCCAT CTTTAAAAT	200
15	ATTTAAAATA TTTTCAAGGA TAAAAGTATT ATCT	234

(2) INFORMATION FOR SEQ ID :973:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :973:

30	TTTTCATCTA AAGGAGAGAG GCAGGCTCAG CTCCTGAAGG TCGCAGAGCC	50
	TCAGTAGTCC TCCTGAGTGC GTCTAACTAA CTACCATCAA AAAACAAACA	100
	AAAAAACAT CACAAACTG AACTGCCGCC ATCACCCTA CACCAAGTAT	150
35	GTGATTGAAT TATTCAATGA TCTGTTTTCG CGGTAGTGAC CAACANC	197

(2) INFORMATION FOR SEQ ID :974:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid

493

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :974:

AGCAGGAGAT TTTTTTAATA ATAAACANCA ATGGAGAGGT GGAAATAGAG 50

10 ATGGAAAAAC AGGATCAAAG GAGCAACATA TCCAGTGA CT TAAAAAATA 100

ATCACACGTG GCAAGAAGTT TTCTAAAGTA AACTGTATGT GGGGAGAAGC 150

ATACAGAAAA AAACGAAATA CATAACCCCC CAGGTTTGAA AGAAAATAAT 200

15

TTTGAGTTGT ATCAATCTAT CGATATCAAA GAATGAATGA CCGC 244

(2) INFORMATION FOR SEQ ID :975:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :975:

30 TTTTTTTTTC TGAACACTTT GCTTCACACC TTCTCATATT CACGGTTATG 50

AATTCTCCTG ACTATATCTA TTGTAACCCA AAACAGCAGA CTGTATTTAG 100

AGACCCATTA GAGATTTCAT GTCTATATGC CCAGAGCCTG ATATAATGCC 150

35

ACCTTACTAT ACACATAATA TAGAATCTGA GGACTACGTT AACTGATACA 200

TGTTAAGTAT CCTGCAGAGA GCTGGCACAT TGAATGTGCT CAATAATCGT 250

40 TAGCTTTAAG TATCTACCTC AAAGGGCTAC TGTGTGACTC CAATGAGATA 300

ATGTGCAATG AAGGGTTTCG TGTAATATTG 330

494

(2) INFORMATION FOR SEQ ID :976:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :976:

TGGTGAAAGG AATAAGCAAC TCAAGGTAAA TAAAGAAGAA AGATGAAGAT 50
15 TCTTAGAATC GTAGAAAGAC TGCAGGGGGA AATAATTAAA GCAGCTTTAT 100
TCCTTACGGC ATTCATCATT CGTCGAGCTG GAAAGCACTG ACAACTTTGT 150
AATGAGTTTT TTGCGCTTAA CTCTGTCAGG TGATTATAT GAATNACTTA 200

20

(2) INFORMATION FOR SEQ ID :977:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :977:

AAAGGACAAT TTAATATAAA TCTATGTTTG TGCATTTCTG ACAGGCCATT 50
35 ATTATCTGCT TTGACAAAGC CTTTCTGAAA CGCAGTGTAC AATGAATCTT 100
AATGATGTTA TGAAACGAGC TTGCT. 3 GCTCTTGATT GGAGCTTCCG 150
GTATGTGATG ACGGTATGTC ATGTATGCAT GGATGTAC. 3 AACTGTGTTT 200
40 AATACTCTGA ATTTTAATTA GAAAAAATA CAATAGCAGC AAGGCCCTGG 250

40

495

TTTCTAAGCT GCATACTTTT ACTAACGCGG GACATGAGCA AATGCC

296

(2) INFORMATION FOR SEQ ID :978:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 10

(xi) SEQUENCE DESCRIPTION: SEQ ID :978:

15 GAATCNCGCC TGACACATAG AATGCATAAA CGAGGGGGGT CCTTCTGCAG 50

ATACTCTAAT CACTACACAG CTTTCTCTAT AAAACTACCC ATAAGCCTTT 100

AACCTTTAGA GAAAAATGAA AAAGGTTAAT GCTTGGGAAGC CGGGGGAGGA 150

20 CTGACCACTT CATAAGCCAG TACGTCTGAG CTGAGTATGC CCCCAGAATC 200

CAGCCACTAC TGATAATTCA CAACGGTA 228

25 (2) INFORMATION FOR SEQ ID :979:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 171 base pairs
 - (B) TYPE: nucleic acid
 - 30 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :979:

CGTACAAAAG CGCTTTGGAG ATGCCAGAAA AAACCCTACG GGAGGGTTAT 50

CCCCCTGACG CTAGGCCATG ACACAACTAA ACTTCAATAC ACCAGGACTA 100

40 AGGCAAGTAT GAAGAAGCAA AATATCGTAA CGACGCACCC TCGAGATCTA 150

496

CCAGGCAAAA CCAGAACCTG A

171

(2) INFORMATION FOR SEQ ID :980:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :980:

15 TGATTCCCCA TTCCTGGA CAGGCAGAG TCAAGCCGAG AAGGAGGAGC 50
CACAGGCCAG CTGTTAATGA GACTAAT AAAACGTTCA GTATTCATAC 100
CTGTGGAACA TGGGTGAACC TTTCTGGTAA CTCGATTTTT CACACCAATG 150
20 ACAGCAAATG AGAAAGTGAG AGAAGCTAGA TAAATGTTTT TAAAGCATTG 200
CTGCAGTGGG AAATAACTGC ACTCTCAGGA CACAGCACTG T 241

25 (2) INFORMATION FOR SEQ ID :981:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :981:

TCACTGCAAT CACGGTAGCT TCGCCCATG CCTCTTCAAC CAGGCACATA 50
CATCGAGAAG TTGAACCTGC ACTTTATTTT AACTGAACA GACTTACCCC 100
40 GACAACAACA CCTCCCCAGT GGGACAAACC TACCCACCT CCCCACACTC 150

497

TACTCCCAGC TAACGTTCCC TATAATCATC ATGACCCATT AACATTGTC 200

AAAACCACAC TTCAACCCAC AGGAAGA 227

5 (2) INFORMATION FOR SEQ ID :982:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :982:

CGTTGTCGCC ATGGTAATAC CGCTCAGTAC GGGAGGACCC ACAGGCTAAG 50

ACACTCGGAG CACGAGCTCG CCTGAGGGAC CAACGAGGCG AAGCCACAAT 100

20 CCGCGAACTC ATGACTGACC CTTCTAAGT AAGAATCCCA CCCAGGCAAA 150

CCAATCCGAC AACCGAAATA GCGCAGGCAC CGCCAAATTC AAGGCGCCCC 200

25 AAAAG 205

(2) INFORMATION FOR SEQ ID :983:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :983:

AGCAACCGGC ACTCAAGTGG AATCCCGAAA AAGTGATTAA AAAATGATCT 50

40 TACCTGTACC AGAAAAGCAA AATTAAAGGA AACAAAATAA GAACCATAGT 100

498

CCCAAATGAC ATTTAACCGT ACATACAGCG ATAACATGTT CAAAATCCAA 150
CAAATAACGC AACTTCCAGA CGTAAATATC CGCCACTCGA TTCCCTCCCC 200
5 CCCT 204

(2) INFORMATION FOR SEQ ID :984:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :984:

ATTTGTATTA GAAAAGTAAA GTTGAAGGAA ATAAAATTG CATCTTGTT 50
20 TTAAGTGATC TTTAATTGTA TATATCGCGG TAGTATGTTT AAAATCCACT 100
AAGTACTGTG ACTTTTAGCT GCAAATCTTT GCTCTTGCT TTTTTTTTC 150
25 TTTCTCCCCC CTCCCCAG 168

(2) INFORMATION FOR SEQ ID :985:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :985:

CTCAGCTGGA ATGTCCGGTG CCTGCTAGGT GCATGGCCAA AGAAGCATGG 50
40 GCTGGGCCTG GGCACAGGAG GAGCAGCTGC TTTGGTCGGG GTGGAGACTT 100

499

TTTTTTTTTT TCTACCCACA GCCTATTCCA CTCCTCCCCA TCTCCAGGCG 150
CTGGGAGGGG GGGCCTCACC CCGTCACGCC TCGCTCCCTC CTGGCCCTCT 200
5 GGTCCAGCCC CTTACGCCTC CTCTCAGTCT ACTCAATTGT GACTGTCCCT 250
CCTGATGTAT TTTTTTTTCC TCCAAC TCAA AAGGCAAAAA TAATCCTATT 300
TTTATTATCT TGCTACAAC T GCAACTTTCT GCCCTATAAA TTTACATTCC 350
10

(2) INFORMATION FOR SEQ ID :986:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :986:

AGCGACCGCC ACTCACTGTG AGTTCCACTT AATTCAGGTG AGCCGCTCTT 50
25 CTGCACCTCC TCCTCACACC TCTCTACCTA TACTAACCAT TTTTGAAGGT 100
TCAACAATGC TCTGCAAATC TTTTAAAGAC CCGTTACTTC AACAACTCCC 150
AATACCTTCC TCCTCAACGG AACAACTTAA CCGTTACCTT TTAACCCGA 200
30 CGAGCTACAA AGCAAGAGAT ACTTCGCGAG CCAAATTCTA CAAAGGACCA 250
AAAAAGAAAC CCATTACCTT ATAGTACTCA TGCAAAAAA 289

35

(2) INFORMATION FOR SEQ ID :987:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

500

(xi) SEQUENCE DESCRIPTION: SEQ ID :987:

5 CACAATCATA GCATTTATTA CAGGATTAC ATCTGATCCT CACGCAATTT 50
TCTTCCTCAC CAATAAGAA CTAATAGGAC AGCATATTAG AAGCAACATA 100
CATTCTTTTA TTCTTGCATC GCTATAAAGA AGTA 134

10 (2) INFORMATION FOR SEQ ID :988:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :988:

TTCTGAAATG AAGGTTTCGT CTTAGCTAT TGACTGTAGG ATTTGTAATT 50
CAAATCATCA CAGCATCCTA AAGAAATACT GTGTGAATGG AATGCACACA 100
25 ATTCTACAG AACACACAAA CTGATGTCCA AAAGGCACAG AGTAATGCTG 150
GTGGCTCTTT CTAGTCAGTT AAGAAACAAT AAAAAGTCTG CATTATTCTT 200
30 TCATAATTTA AATACTTAAG TAATCTCCAC TTTATTATTT TATAACAATG 250
ACTTCAAATT TACATTATTT TAAGTACCAT TGTAATC 287

(2) INFORMATION FOR SEQ ID :989:

35

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

501

(xi) SEQUENCE DESCRIPTION: SEQ ID :989:

AGCAACCAAC ACTCACTGGA ATCCCCGAAT CAAGAGCTAA AAGGACTTCT 50
5 TCCATCTCTC AGGGACACAC ATCCACCGAT AAGAATAAAA GAAATGCCTG 100
AATGACTCTC ACTGGCACTT TTAAACACAG CAAGCCCAAC ATATTTTCTC 150
CTTTTCATAA AGAAGCCTAT ACACCAT 177

10

(2) INFORMATION FOR SEQ ID :990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :990:

TTCCTATACT ATGTCGGTTA AAAGCCTTCA TAGAATATAG GCACCAAAAA 50
25 TAAACTAACC CCACACCCTC ACCAACCAAA GGAGGCACAA TCCAACGAAA 100
CTGATGAAAA GTCGAGGTAA CGACTCTGCA GACCGTACTC ATTTCTAAAC 150
CAAAAGTC 158

30

(2) INFORMATION FOR SEQ ID :991:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :991:

502

	TAATCCCTTT TAAGCAGAGA TACACATTCA CAGAGAGAGA ATGTTTTTAA	50
	AAGACCCACA AGGGGAAGGG ACCAAGTAAG CACTTTTAAT TCATTTTGAT	100
5	TACACAAAA TAAGGCAAAC TAAATGATTC AGAACAATTC AATTAACTG	150
	AAGCCTTCTA GAAAAATACT CAACAGGCTT CAACAAAAAG ACTTAGCGCA	200
	CATAAACAA TCACGAAGAT CACAATTTC GCACAAATAT CTGAAGGAAT	250
10	ACACGCAAAA CATCATA	267

(2) INFORMATION FOR SEQ ID :992:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 199 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :992:

25	AGGATGTGTT CATGCTGGCT TTCAGGATGT CCCAAGGCAC GGCACAGTGA	50
	TTGTCAAATT CCACTTTGCA TGGAAGACAG CACAGAACCC TGCTCTGCGT	100
	CAGCTGGAGA GCTCCGGCCA GCACGGCCAC CAGCAGCATG ATCAGTGTGA	150
30	TGCAATACCA GAAGCCGTCC CACCATGATT TTAAGATGTG ATAAGATGA	199

(2) INFORMATION FOR SEQ ID :993:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

503

(xi) SEQUENCE DESCRIPTION: SEQ ID :993:

TTTAAGGTGC TAAACTTGCA CCTCATGTCC ACTCAGTAAC AAGTATTGGG 50
5 ACGTAGAGCA CAGCCTCACT CAGCTCTGAA AGGTAATACA GCTTGCGAGG 100
AAGTGAGCCA GCAGTGGCCT TTGCAATTGT GGATCTTGAG CTTTGCTCTT 150
AGCAGATCTC AGGCGTAACC ATTGCTAAC TGTACTGAAG ATGCGTCC 198
10

(2) INFORMATION FOR SEQ ID :994:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :994:

GCTATCTGCG GGGCCATTCG TAGGATGGGT GAGTCAGATG ATTCCATTCT 50
25 CCGATTGACC AAGGCCGATG GCATCGTCTC AAAGAACTTT TGA CTGGAGA 100
GAATAACAGA CGTGAATAT TTGTCATAAA TAAATAACGA AAACCTAAAA 150
AAAAAAAAA ACAACAAACC CCAACAAACT CAA 183
30

(2) INFORMATION FOR SEQ ID :995:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :995:

504

ACCTCTGCAT TAACACTCCA GCACCTTTGG TTAGCCAATT TGGCCTTATT 50
TGTGTCTCCA CCATTGGATT ATCTGTCCAT CAAGGTCAGG AATGTTTTCG 100
5 GGTTACCCCA CTGTCCCCAA CTCGAATAT GCTCACTGCC TGGAAAATGT 150
TTATCTGAAT ATAAGGCATC AAGCCAGAAC TTGCCCAAAA CTAAATCTA 199

(2) INFORMATION FOR SEQ ID :996:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :996:

20

GGTCTTGGCT GGTGGTTTAT GGCCCGGGCC TTCTTTCTAC GGGGGCCAGG 50
GTCCAATTTT CCACCTGGGG TTAAAGTT AAGGAGGACC AGCCTGGGAA 100
25 CCCCTCGAGT GGGGACGCCA TTTCTATTAC CAGGGCCCCC TTATATTTTA 150
AGGGGACACC ATATGGAGAT TTTATGC 177

(2) INFORMATION FOR SEQ ID :997:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :997:

40

GAGTTTCCTG TGCTGTTACA AATGTAACAT TCTCATATAC AACATTCATT 50

505

GAAGAGGCAC AATTCTTATT TTGAGGTGGC ACAGATTAGA CAAATTTTTC 100
AGTGAATAAT TCCTCTTTCA TTAGGAAATT TAACCACAAG CTGTATTTTC 150
5 GTAGAAAGTT GCTTGAAATT CTTTTCCTAA AAAAATTTAA TTTTCTATC 200
TCAAAATGAC CGTATGCAAA CGAACATTA 229

(2) INFORMATION FOR SEQ ID :998:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :998:

20

TTGCAGTGTT TATGCCCCGCC TTCTTTCACG GGCAGGTTCATTTCACTGG 50
TTTAAAAGTA AGAGACAGGC TGAACCCTTC GTGGAGCCAT TTCATTACAG 100
25 GTCCCTTAAT TTAAGGAACA AGTTGATTTA TGCTACCTTT TTGCACGGTT 150
TAGGGTACCG CGGCCGTAA ACATGTGTTT ACTGGGCCAG GCGGTGCCTC 200
TTAATATCCG GGGATGTCCA GAAGGGGAGT TTT 233

30

(2) INFORMATION FOR SEQ ID :999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :999:

506

TCAAAACTC AATATAATAT GTAAATCAGG GGTGTCCAAT CTTTGGCTT 50
CCCTAGGCCA TACTGGTGTT AGGCCACATT CAAAGCTATC CTAGGCCACA 100
5 TGTGGCTGGT GGGCCATGGG TTGGACAAGC TTGATGTAA TAAAACCACC 150
AGTGGAAGA GTTTGTTGTG AGTTACATTC AAATACAACA GGAGTAATAC 200
TATCATGATA TTAGTT 216

10

(2) INFORMATION FOR SEQ ID :1000:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1000:

GACAAGACCT AGAAGCAACA ATGCCAGTA GAAACAAACA CACCTACTGC 50
25 CTGGATCTTA GTTTTAATT ATATTCCCA ATAAAGAGAC CCAGGGCTCC 100
TTGTTGAAAT GGCTGATTCT AGGACTGGGG CAGGAAATAT GCAAGATGAA 150
CCTAGAATAT CTAATACTGC CAAAATTAA GAAAGTGTC TAAAAAAT 200
30 CCCCACGGAT AGGGTGTCAA AAGAGACATA GAAGCATCT GAAGGAGTTC 250
CCAATGGCCA AAGATCAAAT AATTTTCAA 280

35

(2) INFORMATION FOR SEQ ID :1001:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

507

(xi) SEQUENCE DESCRIPTION: SEQ ID :1001:

	TGCATGATAG GAGCGTCCTT TGTTCATG AGGTGACTCT TGGTGGGCTC	50
5	CTTATTTGGG GACTGGTCAC CAAAATACC TAACTATGGT TGAAGCTTA	100
	GTGCTTTCAG CCCCATTCCT CATCCTCTGG AAAGGGGAGC AGAGCTGGAG	150
10	CTCGATCATG CCTGCGTGAC AAAGCCTCCA GAAAATCCT TGAAAGACAG	200
	GACATGGAGA GGCTGCTGGG TTGGCGAACA CAGCCATGTG CCGGGAGGAT	250
	GGTGCACCCC AACTCCACAA GGACCCTTCC AGACCTCACC TGTGTATCTC	300
15	TTCATCTGGC GTTCATTG TATC	324

(2) INFORMATION FOR SEQ ID :1002:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 254 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1002:

30	ATTTCATTG ATAAGTCTC ACAAACCCAC TTTCTCTT GCCTGAGTGC	50
	CTCACATACC CTACTGCCTG AGATGGTTCC AGAGGCGGTC TCCTCTCTCC	100
	CCCAACGAAA CACCAGGCAC ACACCTGCCC CCAGTCTTGC CTGCACTCTC	150
35	CTTCTCTCC GCAGAGAGGC ATTCCTTTCT CCTCCTCTCA TCCTACACAC	200
	ACTATAAGAG ACAACTGAAA TCTTGCTTCC TCCAGCAAGC TTCTTAATTC	250
40	ATTT	254

(2) INFORMATION FOR SEQ ID :1003:

508

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1003:

10

AAGGTTGCGC TGCCCATCCT CTCGCCCTTC GGAATTTACC CCTGGCCGCT 50
CAGGGTCTCG CTTCTAGAAG AAGATGATGG ATACTAGGGC GATCCTCCTA 100
TTGCCTTTAT ATTTAACAGG CCCGCCGAGG AGGGGCTCCC GCTGGTGCCC 150
ACATAACTCT ATTAGACCAT CTGAGGCGAC TTCCCCCACC CCCTCCAACG 200
CGCCTCACGC ACGACTCTAG CAAAAGACAG GTTCCGCGGT GGTCACGTCG 250
TTTGAGACTA TACTG 265

20

(2) INFORMATION FOR SEQ ID :1004:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1004:

35

AAATATGCCC TGAGGATTAT CTGATGTGGA TGGTGTGGAA AAGAACTCCA 50
GCAGGCGACT TGGATTCAA TCAATGTCCC CTGAATGCCA CAGAACCACT 100
AGCAGACGCT GCTCTCTCAG TCTTAATGGA GTGGCCTTCT GGGAACAGCC 150
GAGCTTTGAA AGATGCATAT CAAATGAGTA CAGACACTTG TAGCATTAA 200

40

509

TCAAAGAGCA CCTTGCTAAG AGGCAGCGAA TGCTGGCAGG TGATGGAATG 250

CCCCAGGTGA CCA 263

5 (2) INFORMATION FOR SEQ ID :1005:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1005:

CGAGACTGCA GTACTTCTAG AAAGTTGTGA ACTTCTAAGA AAGAGCCAGG 50

CTTCCATCTC ACTATTCCTT GATCATTATC TCTGAAGTCC CTACCTGCAC 100

20 TTCCCTGATT GTCCTGTAGC AACACCAGCA TGGTGGGAAT TGCAGGCAAA 150

GATTGTGAAA AATCCCTAAA GGGTCATTGC TCATGACGTT ATTTCGAATT 200

25 GTAAATCGT GAGCCACTCA TATTCAAAC TAAAAAAGAA CAGAACTTTT 250

ATTCACGTTG TGAAGCTTAC TCCCTCGCCA TTTTACGGAT CAATGTCAAA 300

CGCTTGCATT CATAAAG 317

30

(2) INFORMATION FOR SEQ ID :1006:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1006:

510

CGGAAGCATT ATCCTGTCAT CAGAAGATGG ACCTTTCCTT GGAATGCCTT 50
TTCCCTATCA TGTCTGTGTG GTAAATACCT ATTCATCCTT AACAACTAG 100
5 CTGAGGTCTT ACCTCATCAG GATTTGATCC CCCAAAAAGA TTTGTCCCTC 150
TCTGAGCTAT CTTTATAACT AGTACATACT CCTACCAGCG GACTATGTTA 200
TAATAATGTG GCTATATGCC TGTGATCTCA GCGTGAGCTC TTTGAGGACA 250
10 GAGTCTTTGT CTAAATACTC AAAACCCTGT TTACCAT 287

(2) INFORMATION FOR SEQ ID :1007:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1007:

25 GGGCACCAAA ATACACATCA GAGGAGACTG GCTTCCATGA GACGCTTCGA 50
CTGTCTCATC GGGGCACTTG TAATAAGCAT CTTGATGCCA CTGAATGCAA 100
TGCTGTATTC AAATAATAGC TTTCATCTTC ACTATAAAAC AATACAAACG 150
30 TAAACTTTGA AGCCCTTTGA AGGACCTAAC CAAACAACAC AAGGATGAAA 200
ATAGATCAGT ACAACTTTGA GACACATTAT TAGGTCAAAT CTGCAAAGCA 250
35 TATTCGGATT TTACCGTAAG GAA 273

(2) INFORMATION FOR SEQ ID :1008:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

511

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1008:

TAGAGTGGGG GGCCAAAACC TCTGCAGTCC CCGGCAGTGA GCTATGGACT 50
TTCTTCCCCC TCACAAGGCT GGGGGCCTCC TGCTCTCGTC CCTGGCCCTC 100
10 CCTGCACAGG GCAAAGCCAG TCTGGGCTAT GGCACACAGA GTTCATGTTT 150
GCGCCCTCTC CCTGCCCCTC ACCCCAGAGG GTGAGGAGGA ATGAGGGGCA 200
15 TTGATGGTTA GGCCGGTTGT TGCCTCGAAC AGCTGGAGGG AAGCTGCAGG 250
GGTGATAAAA TCAAAGCGAT ATTGACACAC TACAAACATT ATAGAACCTG 300
CAAAAAAA 308

20

(2) INFORMATION FOR SEQ ID :1009:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1009:

GAACCGCCTC TGTTTCCAGA GCAACTGGTC AAAACCTCTC CAAATACCGA 50
35 GCAGTTTGA AAACTGGATT AGGAACCACT AATGAAAAAG AACAGACTCA 100
GGGACAAGTG TTTGGCGGGA ATGTGTGAAG AGGTAATAA TGAGTGTCAC 150
TGAATCACAC TATTACACAG ATGAAACAAA GCCTTTA 187

40

(2) INFORMATION FOR SEQ ID :1010:

512

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1010:

10

AAGAAAAGA TATTAAGATG GGCAAGTCCT GGTGGCAAGA CAAGCAGATG 50
ACATTACAGA CAATGGACAT CAAACTGCTG CCAAGCTAAT TTAGATTGTA 100
AAAACAGCTC CATAGTCAAT ACCCATGAGT GATCTTAAAT ACGCACAATT 150
AAGCTACTTC TCCTTGATAT TACCT 175

15

(2) INFORMATION FOR SEQ ID :1011:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1011:

30

TGAAAAATAT TTGGAAGTCT TTAGTACAGA ACAGTTTCAA TATGAGTTAA 50
GAATCATGCG ATGACTACCA AAAAGCTAAT GCGATCCCAG GCTGCGGTAA 100
CAGAAGCAGA GCAGCTCAGC TGGGGAACGT GATAGTGATA ACTACTTCGT 150
ACTAGGTTAG ACTGTACCGA GAGACCTATG TTCAGTTCTG GGAGTGAAAG 200
TATTTTAT 208

35

40

(2) INFORMATION FOR SEQ ID :1012:

513

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1012:

10

ATGATATCTA GACTACCACT ATTTTTTGAA TGAGGCTTTC TTAGGAGTAT 50
GTTGATGCAC TCTCATCCTT TCCTCCCCGG ACTCCTACCA CAACCCTCTG 100
ACTGTGGAAT AGCATGGTTG TGTGTAAGGC TGGAGCACAG GCACAGTGAG 150
ATGAGGATGA GGGATTGAGG GATGCTATAA GCCA 184

(2) INFORMATION FOR SEQ ID :1013:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1013:

30

CTTTGACATT TGATCAGACC AAACAGTGCT GTTCCCGGG GAGGAAACAC 50
ATTTTAATAA ACACATCATC CCGCAGGCTC CCACCTTTAC CTCATGTTTC 100
ATACCTTGTT TATCAAATGA GCGACTCAAA ATGATTAAAA ATAATGCTGT 150
TCTTTAGTAG CAACTAAAAT GTGTCTTACC GTCATTTATA TCTTTGTCAC 200
CGGAAAGAAG CATTTTTGAT ACTTTACTGC GAGTCAAAAA TCAATACGCA 250
GAATGGCATT TGA 263

40

514

(2) INFORMATION FOR SEQ ID :1014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1014:

CAAATTAAGT GCCAGAATGA TGCAGCCCGC TCTCACCAGG AAGAACCACA 50
TGTGAGAAAA CTTATAGCAG ATGCAAAAAT GTCAACCCAC CATGTTATTT 100
AAAAAAAAT ATGACCAGGA TACAAGGACA CTTCACCGTT TTTAACCAC 150
ACAAGGTCAG GTAATGTTTA CCTTGAAACA CAATCGCATA TGACCCTTTA 200
TGCCACTCAC CTAGGCCTTT AATAATGAG 229

(2) INFORMATION FOR SEQ ID :1015:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1015:

GAAAATAATG ATTCATATTA CCGGGTATTT CTTATCCAGT CTTTCATTCT 50
ATGTAAATTG TGTGTGTGTC TATATATGCG TGCATGTCTC TCTCTACATG 100
TATATGTGCA TATGTATGTA TATATATGCA TATGCACATA CATGCCACAC 150
ATGCACATAT ACACACACTC ATAGAGAACA AAATTATTCC GAATATTTC A 200

515

TGAGGTTTCT TATTATAAGG AGACAATATT GATGCAATCT AATTAA

246

(2) INFORMATION FOR SEQ ID :1016:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1016:

15 TTCATAATCG CTGGCACTGA ACAAAGTGC AGAATTCTTT GCCAGGTACT 50

TTAGGAAATC GTGAAGATAA TTGAGTAATA AAGCAAGGCT CTTCTCATCC 100

AGAGGTGTAT AAGCCAACAT CGCTCCAATT CGTACAAATA ATCTCAGGAG 150

20 ATGTGGCGCT CCATACACCT GGGACATGGG TGCATCGGGA TGATCTGCAA 200

GAATTTCAGC ATACTGTGGT CTCTCAAATT TATAGAGTAG CTGGGTACCC 250

25 AACATTACGT TGAAGTATTC TTTTATACTC GCCACAA 287

(2) INFORMATION FOR SEQ ID :1017:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1017:

40 ATATGAGAAA GCAGAGCAAA ACAGATGATG CTCTAAATGC AACTGACACA 50

CTTGCTAAAG ACGTTAGGTG CTCCATAAAT GCTTGTTGAA ATGCTGTTTG 100

516

TCAACATTG TTGTGAAAAA TTCATCTCTC CATCTAAGAA TCCTCATGAG 150
TTAACCACAA TCAGTTCTAC ATAATTTAAC AGAAACATC TGGTGGCACT 200
5 TTTAAATGTT TAAGGACAGC ATTTACAAA CTAAGCCCGC CCCCAGTCCC 250
ACTGCAGCAG GAGAAAATAA GGCTATGGAG AAAAGCAAGA TGAGTTATA 299

(2) INFORMATION FOR SEQ ID :1018:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1018:

20

ATTACTCCTT CTCTCGAATG CTTCCAGAAG AGTAGCACTC ACCACCTCAT 50
GAGGAAAGGC ACTGCAACTT TGGTCAATGA TATCTGTTAG AAAGATCTTT 100
25 TCCTATATTT AGAAGAGTGA TTCTCATACC TGAGCATGTA TGAGAATCAG 150
TGGGTTTGAG GTGGGCCCAA GAATTCCTT TTTAACAAG TTCCCAAG 200
ATGCTGATGT GGCAGCTTCT AGCACAGTGC TTGAAAATCC ATGAGTTTTC 250
30 AAGAGGACAA TCTAAAGTGC TCCC 274

(2) INFORMATION FOR SEQ ID :1019:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

517

(xi) SEQUENCE DESCRIPTION: SEQ ID :1019:

TTTCTTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA 50
5 CAATTCCAAT GTTACGAAGT CCAAAGAAGT GGAATGAGAA AACTCCTCAC 100
GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG 150
CATCTTCTAC CACTTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA 200
10 AAATGGCACC TCATCTTTGA TCAAAGATTC AG 232

(2) INFORMATION FOR SEQ ID :1020:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1020:

25 AACAGTCCAT GCTGATCTTA GTAACATGA TGAAGATGGT GCTTGGCCTG 50
TTCTTCTTGA TGAATTTGTT GAGTGGCAAA AAGTCCGTCA GACATCATAG 100
CAAGAACTAT GTGAAGAAAA TGCAAACCTT TAC 133

30

(2) INFORMATION FOR SEQ ID :1021:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1021:

518

	TCCTAGAACT CTGCTTGGAC CAGAAGATGT GAATAAACTT AAGCTTATTT	0
	ATTTAAAATC ACAAATGAGT TGCTCTAGAT TCTAAAAGGG TGAAACTTTG	100
5	ACTGTTGAAA GTTTAAGTAT TAGTAACTT GAGTTACTTT TTCTTTCAAA	150
	TTTCACTCCG CTTCCCTGCA TTTCGAAGCT GCTCTTTCTG GTCCTACCCA	200
	CCACCCCACC AACAAGACTT GTGTTTGTTA ATAGAAATAA TTTATCAAGG	250
10	TATTGGGGAT CCATTGTCTA TATTTAAAC	280

(2) INFORMATION FOR SEQ ID :1022:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1022:

25	AAAATAAATA ACTTCTTAGA TTTTGGACTG AAAAGATCTG AGAATGTTCT	50
	GCCAAACAGC CGACCAACTG GTGCAAAGG TTAAGGCTGA CTTGACTTAG	100
	CAACCTGCAG CACAACCAA AACACTGATG CAGTTCAGAG CTCTTCAAT	150
30	GCATACTTCA GTGTTACACA CACATCAATT AAATTAGGTT AAATTAGTTA	200
	ATCCTCTAGA CAGTTTTCTT TTTGTTTTGC ATGCATCCCG TTCCATTTTC	250
35	ATTACGGGCA TCTATTCCTT GATCAATTAT GTGCTTTGCT TTTAATCGG	300
	TTTT	304

(2) INFORMATION FOR SEQ ID :1023:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs

519

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1023:

TTTCTTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA 50
10 CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC 100
GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG 150
15 CATCTTCTAC CACTTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA 200
AAATGGCACC TCATCTCTGA TCAAAGATTC AGAGCAT 237

(2) INFORMATION FOR SEQ ID :1024:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1024:

30

GGCATGATTA TTAGAAACTA TTTAAGCTTT TTTCTTTGAA AAACAAGCTC 50
CTTTTACAGA ATATAAACAA CAGTAGTGCC TGTGGTTTAG CCCACCAATC 100
35 TTGATGACTA AAAGTAGCTG ATGCATTGTG CATATGATGC TTGAGATGGT 150
TTTTGCAAAA GCAGAAATCG CTGCAAGGTA ATCACAATAG ATAAAAGTGG 200
TATTTTAAAC CTTTGAAATA AATGGATGTA ACTGTACCTT GGTACAGCTT 250
40 TTCACTTGTT TAGTTTTTAA ACGTTAGTAT AAGATTAGGT AATTGAGGGT 300

520

TAGAGCCAAC AGGAATCTGC

320

(2) INFORMATION FOR SEQ ID :1025:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1025:

15 TTCTGGCACC ACATTCAATA CTGATTCACA GGGATCTAAA ACATTCTAGT 50
TATTCAGTCA CTCTGTCCTG TGTGGCAGAT AGGACTTATG TATCTTCAGA 100
ATATTTGAGG AGTCATTCTC AGAGTCTCTC ATGAGTGCTC AACTTAACTG 150
20 TTCCACAAGT CTGTCTTCAT AGCTGCATGT TGCATCTTCC AGTCTCTGTT 200
CT 202

25 (2) INFORMATION FOR SEQ ID :1026:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1026:

ATTGGTAGAC AATATCATAA GAGTTTTCTG ATAAAAGATG CTTTTTAACC 50
CTGACTCCCA GTCACAATTT TGGCATCTCA TCCATGGGAA AAAAATAGGA 100
40 AACTTATACA TTTTATAAAC TAAAGGTCAT CCAAACACTG CCAAAAACGT 150

521

TTTTATAAAT TGAGACCTAC TTACATCACA TCGGTTTTCC AAAGAGAATA 200

CACAGCGAAA GATGAGGCTC CACCCGGCCG GCACAGTCAT GAA 243

5 (2) INFORMATION FOR SEQ ID :1027:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1027:

TATTTGCATT GAGGAAATAT TAATTTTCCA ATGCACAGTT GCCACATTTA 50

GTCCTGACTG TAGGAAACAC TGATTTTGTA AAGTTGCCTT TATTTGCTGT 100

20 TAACTGTTAA CTATGACAGA TATATTTAAG CCTTATAAAC CAATCTTAAA 150

CATAATAAAT CACACATTCA GTTTTAAAAA AAAAA 185

25 (2) INFORMATION FOR SEQ ID :1028:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1028:

GCTTCTCTAT TCCTCCTGCC CGGGAGGAGT AGAGGAATTC TGGAGCCACC 50

TTAGTGGGCA ATGGGGGAGC TCCTGATGGT TCAGGAGCAG GAAATTTATG 100

40 AGCAGAGTGG GGTCCCAGGC CACAGGGAGA TGTCTATCCA CAAGGGATGG 150

522

TGGCCAAGGG TTGAATGGAA AGAGGCAGGC AGGGGGAGAG GGGCAGAGGG 200
TGTGGGTATT CCCAGGGCCT TGAGAGTGGA CATGGCCCCT TCTCCTCAGC 250
5 CTTCCATTAG CAAGGATGTC ACTGCTGCTC TTGCCTGATG ACAGCCAGAT 300
CTGTTACAG TT 312

(2) INFORMATION FOR SEQ ID :1029:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1029:

20

ATTATTTATA AATTTTAGTG AGCACCACCA AAGTTAGGAT TCAATTGAGT 50
TTGAATTCAA ATTCATTCAA AAGTTGCACA AATTATTTT TTTTTCCTG 100
25 AACATTCCTT TACTTCAGAT TGACAATTCA TTCTATTTAG AGCGCTATTT 150
TAAGAAACCT TGATGAATCG CCCTTGACTA AAGGAAACAA AGTAGAATTT 200
TATACAGATG GAAAAAGA 218

30

(2) INFORMATION FOR SEQ ID :1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1030:

523

TTATTAGGGG GTTTAGAAAA TAAATTCGTA GGGTTTAAAC ATTGAATAAA 50
ACTACAAAAA AAGACACACA TTCAGGTAGC GAGGCTCTGG GGGTAACTCT 100
5 TTCTTAGTTC TTTGGACACA TCCG 124

(2) INFORMATION FOR SEQ ID :1031:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1031:

TTTTGCCAAG TATATGTAGT GCAAATATTT TCTTCAGTC TGTAGCTTGC 50
20 CTTTTTATTT NTTAATGGGT ATCTTTAAAA AAATGGAAGT TTTAAGTTTG 100
AATGGAATTC AGTTTGTTTT TAAAGCTTGT GCTTTTGTG TTCAACTAAG 150
25 GGATATTAGC TTACCATTTT TCTCGGTGA ATATTATGTG TTTATAGACA 200
AGAAATGGTC ACTAAAGCAA AATACTGAA AATTATC 237

(2) INFORMATION FOR SEQ ID :1032:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1032:

40

ACAGCAACCG GCACTCACTT GGAATCCCAG TGTTCGAGT TCTAAGGCCA 50

524

CTGAAAACCA TCAAGCGCTT GCCAAGCTCA AGGCCATCTT CGACTGCGCA 100

GCGACTTCCT TGAAGACTGT TTTAACATA CCAAAGGAGG ACAAGCT 147

5 (2) INFORMATION FOR SEQ ID :1033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double.

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1033:

AGGCCTGCCT ACCGTAGGTC TCTCAGAGCC TTTACTCTAG TCACTCTTTA 50

GAGGGGGGCA CTAGAAGCAA TATCTCCGAA ACTTCTTCGA CTGTCGAGAC 100

20 TTTTACTCA TAATTCGCTT CAAGCCAACT ACGGAGGCGC ATTTACAAAA 150

CTGAAATACG AGCGACACCC CAGGAACGCA CGGAGACATG ACGCCCTTAA 200

25 TCCTCTGTCC CTACTCCCTC TCCTAGGACA CCGCATTA 238

(2) INFORMATION FOR SEQ ID :1034:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1034:

TCCATGNCTC NTGGTCTCTG TGCNCTTGNC AGGGGCATGC CAGGGCCCTT 50

40

GGACTGTGCA GGG 63

525

(2) INFORMATION FOR SEQ ID :1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1035:

CGACCGGCGC TCAATGGCGA AATCCGAGC CAGAGCTATT GGTGAATGA 50
GTAGCGCTGA TGGTTTAGAT AATACTAGT ATGGGGATAA GGGTGAGCAG 100
GCGCGCCTTG AGGCAAGAAG CGGGTTAGAG CATCTCTACT TTAAAGCCA 150
AAGCCTATAA CGGTAGCGTC TACATCACGA 180

20

(2) INFORMATION FOR SEQ ID :1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1036:

CCAAATACGA TGACATCAAG GAGTCGATCC GTCAGCGTGA CTTGAATACA 50
CCACCGCCGA CGACCCGAAA GCCTGATGAG GAGAAGTCCA GAATCAGGAA 100
CAACGGCGAC ACTCGACTAA CCATTTTAAA CCAATTGGAA CC 142

35

(2) INFORMATION FOR SEQ ID :1037:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs

526

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1037:

CCACATGGAG TGACCTGGGC CTCTGCAAGA AGCGCCCGAA GCCTGGAGGC 50
10 TGATTGTCAA AGCAGGGGGC AGGACCCGGG GGCAGGAGAA ACCAG 95

(2) INFORMATION FOR SEQ ID :1038:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1038:

25 ATTTTATTGT AGTAAGAATA ATACATAGAA ATAACATTAA ATAAATATGT 50
TTGACAAAAA CATAACACA TAGTACAGGT AGAACATATA ACTGGTTGAT 100
GCTAAATAAC AGATCCAGAT AATTTTCAAT TTGAATTAGC AGCAGGGAGT 150
30 CATTGAATGC TATGCCCTTA GAATGGCTTG CAGGCTTTCA CGAGT 195

(2) INFORMATION FOR SEQ ID :1039:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

527

(xi) SEQUENCE DESCRIPTION: SEQ ID :1039:

	GGTTGTCAAG AAAATGAAAG GTAAAGCTCA GAAGGGATAA GGGAAGACAT	50
5	TACAGAATTT ATCATCAAGC AGGAGGTTTT TTCCAGGTTC TAAGATGAGG	100
	TTAAGTTTCT TAACAAAAGA ATAAACAACT GTGACTCTAT CTGTCGGGGG	150
	AGGGTCTAGA CAGAAAAAAT GAATATACCC CAAAAGGCTG AAAAAAAAAA	200
10	CGAGACTTTG ATGGAGAC	218

(2) INFORMATION FOR SEQ ID :1040:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 318 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1040:

25	TTTATTATTT TGAATGATTT AATGGTTTTT TACACAATTT ACATCACAAC	50
	ATGTAAATTT TAGCAGTAAC ATCTGATTCT AACAGCACAT CATGCTATTC	100
	CTTTCATAGA GCCTTCAGAG ATTCAATGCT AAACAAATTT CCTTAGTTGG	150
30	CATCAAGGCA CTGATCACTT TAGAGGCTTT TAAGAAATTA TTTAAAGATG	200
	CAAATGCCTC TGAGTGAAGT GTACTATCCC ATCACTGAAG CCCACAGGAA	250
35	CAAGTCCTAC AATTTTAAAA AGGCTCGATG GAAAAATTC TCAATCCTGA	300
	AATCCCCTAG GGAAGGGG	318

(2) INFORMATION FOR SEQ ID :1041:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 199 base pairs

528

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1041:

ACGTACCGAG CCGTCGTCGC GGTGCTTGAG CTTGAAGGCG AGATAGCCGA	50
10 TGCCGCCGAG GCGGTGGACC GCATCACGGT GGCGCTGACG AACGCGAGAT	100
TCAGCAGCAG CGATGCCATC AATAGCAGCC TGATCGGACG CATGACCGAC	150
15 TCTCCCTGTG AGCGGAGGTT GGGGGGCCGA TCTCCCGCCG GTGCCGGGC	199

(2) INFORMATION FOR SEQ ID :1042:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 300 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1042:

GCCTCTAACA AAAGTAGGCT GTCCCGGACC ATGGTAATAG AATTGTTTAC	50
30 CTTTATACCA AGAAGGTTGG GAAAGCACCA AAATCTGCAT GTGGTGTGTG	100
CCCAGGCAGA CTTGAGGGG TTCGTGCTGT AAGACCTAAA GTTCTTATAG	150
35 ATTGTCCAAA ACAAGAAAC ATGTCAGCAG GGCCTATGGT GGTTCATGT	200
GTGCTAAATG TGTCGTGAC AGGATCAAGC GTGCTTTCCT TATCGAGGAG	250
CAGAAAATTC GTTGTGAAAG TGTTGAAGGC ACAAGGCACA ATGTCTGGAA	300

40

(2) INFORMATION FOR SEQ ID :1043:

529

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1043:

10 GAGACCAGTC TCAAGTGGGA GGGGCTGATG GTGGGAAGCC CTAGAAGAGA 50
GTCTGGGATG AAGCGGCCTC CTCCTGTCT TGGCCTCCAA AATTGAGTCT 100
15 GGCCTGATTC CTTTGAGGAG CAAATTTTAC AATCATCCCT CACCCTAACA 150
CACGGTGAAA CTGGAACACC 170

(2) INFORMATION FOR SEQ ID :1044:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1044:

30

GGCCCCCCT GGGGACTGCT GGTTTCCAGG GGCCACCCCC CTCATCCAA 50
AAGAAGAATC AAGTTTTGTT TTCCTGTGGT TCCCTTGCTC TCCCCGGCCT 100
35 CACCTCGAGC TTCCAATTGG GCCCTTTCCC ATGCTTCTAC TTGAGCCCCG 150
CCTGCCTCAC CGTCTGCCTC ACCGCCACCT CCTGCTCAGA GTGAGTGCAT 200
GCATGCCAGA CAGATACACA TATACATACA CACACACACA CACACCCTAT 250
40 TTTTTTTTTT 260

530

(2) INFORMATION FOR SEQ ID :1045:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1045:

AAATCTATAA TTTTAAGGGC TTAACCTGTG ACTTTAATAA GCTGGAACAG 50
15 TCCACTGAAT GGGTATAATG AATTGCAGTA TATACGTATG ATCGCTTTTT 100
AAGTGATTAT CTTTTCTTTC GTTAAGTCAT GTAAATTCAT AAATTTTTTG 150
GCACTGATGT GTTG 164

20

(2) INFORMATION FOR SEQ ID :1046:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1046:

TCCCTCCTTT CCGAACTGGA GCCCCATCCT CTCCAGAGTA TCCAGGGCTT 50
35 CTTCACTCCC GGGTACCTGC CCTTCGGCCC CTTTTCACCA CAGCTGTGCT 100
ACTGTCAACC AGTCTTTGCT GCATAGGCAT 130

(2) INFORMATION FOR SEQ ID :1047:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs

531

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: lin ar

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1047:

10 GCTTAACTGG AAATTGGAAG GGAAAAGAAG AAGAAACAAT GTAATGTAGC 50
AGTGGAAGCA AAATTCTCAC AATGAATAGC AGTCTTTCCA GCTTCTTTGA 100
CACGGATTTT CTCATTAGAA AAGACGACTC TCCTGAACTA GGGATGAGTG 150
15 TGAATCTCCA TTCGAGGAAG GGAAGAAGA GCTCGGAGGG TGACAGCCTC 200
CCCCTGAGAG AGCCAGTTGC GTTCATGATT TTGATTCCTT CTCCTCCTG 250
ATGAAGTATC TGCCCAGGAG CCCAGGAGCA GAATA 285

20

(2) INFORMATION FOR SEQ ID :1048:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1048:

35 TAAAACTGAC CTAGAAGCTA TCAGCAACCA CAAAGAGACA GAAGAAAAGA 50
CTGCTTCTGA GGCTCTCTCA TGGAACCTAC TGATGATGGT AATACCACGC 100
CCAGAAATAA CGGAGTCGAT GATGATGGCA ATGATGACGG CGATGATGAC 150
GGCACTGATG ACCCCAGGCA CAGCGCGAGT GATGACTACT CAACACGAGC 200
40 CAGGTCTTTC TGAAGGCCGA GAGAGCTAAA TAA 233

532

(2) INFORMATION FOR SEQ ID :1049:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1049:

ACTTTAATTT ATTTCGGATG CCGGAATTGT GCCCAGAGTT TCTCCTGAGC 50
15 TTGATTCCAT AGCTAGCAGC TTCAATCCTT CGCAGCTGCG GTGCGTTCTG 100
AACTCTGAGC TGTCTTTCC TGACAGGCAC TTTCCATAGC ATCTGCCTGC 150
TTAATTCCTC ACGACTCAGA AATGTAAACG GCACTGTCTGA GTGCTGTGAT 200
20 CATTTTGCTT TAACTATGTA AAGCTTTATG CCCTTCGAGA AGCTTATTC 250
GAGATAGAGC TAGAGAAGAA AAGCAGCAAA ATTCGGTCTGA TAC 293

25

(2) INFORMATION FOR SEQ ID :1050:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1050:

AAACTATAC TTTCATTCAA AAGAAGAGCT GAATTGATGC TTGAGTTACA 50
GCACAAATCT ATTATTAGTG AATGAAGTAT ATTCTTGGCA GATAAATACC 100
40 AGATCAAAAG TCCTGTTTCA GTAATTTGAT TAAACTGTAG AATACTAAAA 150

533

AATAAGTTAT TTCTACAGAA ATCTTTGAAG GGAGCAAAAA ATCAAATCAC 200

AGTATATACC TAATGGCTA 219

5 (2) INFORMATION FOR SEQ ID :1051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1051:

AGCGACCGGC GCTCAAGTGG AATCCGTGC AGTGTGTTGAT TTTTCGTTTT 50

TGCGATAGTT TACTGAGAAC 70

20

(2) INFORMATION FOR SEQ ID :1052:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1052:

ATTCCTGACC TGTGATATCG GCCATTAGAG CCTTTCAAGA ATGGTACCTC 50

35 CTGCCGATGA TTTTTTTTAA AGCCTTAATG AAGAGAGTGT CCTCTGACTC 100

CTTCCAGAGA AGATAGGATG TGAGTGAGTA AGTTATGTAT AATAATTTTA 150

TCTCAAATA ACCACGTCCT TGATACCATT CCCTGTATAC CAAGGAAGGG 200

40

TATT 204

534

(2) INFORMATION FOR SEQ ID :1053:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1053:

ACTAAACACA GCACTGAGAA TTCTCCTCTT TTTACAAAAA TGACAGACTT 50
15 AAGAGAGGGC ATGGAACAGA TTAAGAGAAT TAACACGGAG AGGAGAGCAG 100
AGGTATAAAA GGTATCCAAG AAAAGTAAAA CATACAAAGG CAATTCAAAT 150
CAAAGTGAGC ACTGCCTATA TACAGACAGA AAGCGAGTCC TCTATGAAAC 200
20 CATACCCGAC AGAAAGTACC GGAATACCAC CGACACTGAT GTCTTCCAAA 250
CG 252

25

(2) INFORMATION FOR SEQ ID :1054:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1054:

AAATCAGGAA ATTGTACATG TTAACAAAAT AGTATAACCA TGCATACATA 50
CATCTGCTTA TTAAACACTG AAGTAAAAGA ACTAATCCAG TTTGCAGTCT 100
40 TTAGAGGTGT TTAGTATTTT ACTCCGTTCT GATGGAAGCA CTTTGAATGC 150

535

TTGCATGGAG ACATAAACT GAATATTTAA TTGACAATAG ATCATGCGCC 200

TGTATTTATA AA 212

5 (2) INFORMATION FOR SEQ ID :1055:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double.

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1055:

ATAAACTGTG CTAATAAAG TTTTATTTTC ATCAATATAA AAGCTGTAAA 50

AAAACCTGAGG AGAAAGCAGT TGCCAAAAG ATGAAAGAAA AACACATAG 100

20 AAAACCTTTA AAACAGGCAA AAGTCAGTTC ATAATAAAGT AACTCATCTC 150

AC 152

25 (2) INFORMATION FOR SEQ ID :1056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1056:

AACAGATCCT CAGTTTCTCT GGAGACACCC CCAATTCTCG GGTGAGTGTT 50

GAAACCTGAC AACTGACTGT TAGCCTTGTC ATCATCCTCA TTGGAGATGG 100

40 AGATGTTGTA GTCGGAGCCT CATTCCTTCC GGGGCACTGT TTCTTCTAAT 150

536

GGCAACCATC AGAGCCTGTC TGGAAACAGC CTGCTGCCTT TGCTAGGGGG 200
GCAAA 205

5 (2) INFORMATION FOR SEQ ID :1057:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1057:

GAGAGAAGAG CGCTTTTCTG GGCTCTTGGT TACTCCGTCA GAGACTTTGC 50
CCTTTGTCTG TTAAATACA CTGGGAGCCA GAGCTGATTC CCCACCTGCT 100
20 GCTGTGGTTT TCCGCTTAAC ACAGGAGAGA TGAGTTGGTC TGGTATATTT 150
GATAGCAGGT TTAAATGA ATCC 174

25 (2) INFORMATION FOR SEQ ID :1058:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1058:

TATTTGATGG TCCATAAGAC TTTGTCAAAT GTAAACCTAC AGTTTGATAA 50
GCTTTAAAAT ACCATGTTGA CAGCATTTTG AATTGTTTCA TAGACGTACT 100
40 TATTTAACTG ATGCGAACAT TCACA 125

537

(2) INFORMATION FOR SEQ ID :1059:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1059:

TTATCTTACA ATTCTACTTC CCAGCATCCT GAAATTTTCA AATACTGTCT 50
15 TAGTATATTA AACTCTTTTG AAATAGATAA CAAAAGCACC ATGGGAGTCC 100
GTTGAAAACT TAGGTTTGTT CCTTCTAAAA TTTCTAAGTC CTCATTATG 150
ACTATAAAGA AAAAAGGTTC ATCAATTCAA AAAAAAATCC TGATTCTTCA 200
20 AAATA 205

(2) INFORMATION FOR SEQ ID :1060:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1060:

35 ATCTCACAGA TTCTTTTTC CAGATTCATT CATGTTGAGT GAAAGAAGCC 50
AGATGCAAGA GTCCACACCA CATGATTCTG TTTCTATACA ACTTAATTTG 100
AAAATAAGC AATACTTACA GAAGTGAGAA TAGTAGTTGT CTCAGGGTAG 150
40 GTGAGTGTCA TGAAGGGAAT CTTATACGTT TGCTAAAAAT GTTTTATAAT 200

538

ACTTGGATT TGGGTCTA 3CTGGCAGG GGAAGGGTA CATTGCAAA 249

(2) INFORMATION FOR SEQ ID :1061:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1061:

15 TAGCACATTG CATCCCAAGA GCTGTAGTCA AAATCCTCAA AATCTGATGA 50
AAATGGCATA CTACACTAAG GAGGATTTTT TGGGCATTTT CCATTCATAT 100
GCAGAATCAG TGTTGAAAA AGGAGAAAGA GAGATTTTCT TTACAAAAGC 150
20 TCCTGACCCC ATTAACATCT TATCTATAAA TCTGATATGT TCCTGACTCC 200

(2) INFORMATION FOR SEQ ID :1062:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1062:

35 GCGCACAGCT GAGAATCTCC GGTCTTGCT CACTTTGGAC TGGGACAGTG 50
GATGCCCATC TAAAAGTTAA GTGTCATTTC TTTTAGATG TTTTACCTTT 100
ACAGCCATAG CTTGATTGCT CAGAGAAATA TGCAGAAGGC AGGATCAAAG 150
40 ACACACAGGA GTCCTTTCTT TTGAAATGGC CACGTGCCAT TGTCTTTCCT 200

539

(2) INFORMATION FOR SEQ ID :1063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1063:

TATCAAATCA TGAGTTGAAA GATTTTGACT ATTGAAAACC AAATTCTAGA 50
ACTTACTATC AGTATTCTTA TTTTCAAAGG AAATAATTTT CTAAATATTT 100
GATTTTCAGA ATCAGTTTTT TAATAGTAAA GTTAACATAC CATATAGATT 150
TTTTTTTACT TTTATATTCT ACTCTGAAGT TATTTTATGC TTTTCTTATC 200
AAATTCAAAT CTCAAAATCA CAGCTCTGAA TCTTAGAGTA TCATAA 246

(2) INFORMATION FOR SEQ ID :1064:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1064:

CCCTCATGTG CCAGTTCGGT CTGCCTGCAG AGGCTGTGGA GGCCGCCAAC 50
AAGGGCGAGT GGGAAGCGTT TGCAAAGCCA TGCAGAACAA CGCGCAAGTT 100
TGAGCAGAAA GAGGGCGACA CGAAGGACAA GAAGGACGAA GAGGAGGACA 150
TGGAGCCTGG ACTGAGCCAC 170

540

(2) INFORMATION FOR SEQ ID :1065:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1065:

CTCTCCCCCA CAGGTTCTCA GCAGTTACTA AGATGTCCCC TGATTTCATT 50
15 GACCTCTGTG TGTCTTCAGT CCTTGACCCT TTAAGGCTCC CTGGTGCCAG 100
AATGTCTGCA GCTGTAGGAT CAAAGACCCT TGGGGGAAAA ATCCATTCTC 150
AAAAGAGAGG AAGATGGGGT G 171

20

(2) INFORMATION FOR SEQ ID :1066:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1066:

GAGTCTATAT CCCTTACTCA GTGCAGTTCT CAAAGTCCTT TGTATGTCGT 50
35 ACAGGATCAC ATCTGTACAT ATCACACTCT TGTGGGGTAA GCCCAGAAGC 100
TCATACACAG CTTTCATGGGT TTACTTTCCC AAGCACTTCC TCCCTCCCTG 150
CAATATCTCC CCAGCACTTT CTGCTTCCTA TCAGCTTTCC CCTTTTTCAA 200
40 C 201

541

(2) INFORMATION FOR SEQ ID :1067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1067:

ATCAACCGGA GGTGAAATGA AATACCGTCA ACCTGTGCAT GAGTTTGTGT 50
GAACTGAATG TGTGTGCATA CACATAAGCA TGTGTGCGAG CGCAAATGTG 100
GCGTCTCCAC AGCATGCGCA ATCCATGAGT CTGTTTCTAA CGCGCGCGCG 150
C 151

20

(2) INFORMATION FOR SEQ ID :1068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1068:

ACTGTGTCAT GTCAGGTTAG ATCTGAATCT CTAGGAGAAT AGCTTTTTTG 50
ATCTGTTTGC TCCTTTGAGT CTCCCTTTTA CTTTACAACT AGAAAACCAA 100
TCGCATACTT CACTTCTATC GCTTCCAGAT ATGGCATATT TTTCTTAGGC 150
TACCGTTGAA ATTTAGCATA ATATTTCTCC CTTACCTTTA CGTCCTTTTA 200
AAAAAATAGG ACTATAGTAA GTCCTCCGTG TCGGTGGCAT GTTTTTGGAA 250

40

542

ACTGACTTTA AAGAAAACAT ACA

273

(2) INFORMATION FOR SEQ ID :1069:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1069:

15 CAATCTTGCT TATAAAATAA GAACACCTTT CAATTAAGTG AGTGGGTCAT 50
TCCTGGTGCA ATTGTGATTT TTTTITAGCC AAAATGAATG GCAAACTCTA 100
TTTAGAGCAA AGTAAGTATT AGAAAACCCT AGGAACTCTT AATCAACGTT 150
20 TATTACACTT TTATAAAGGC AACTACGCG AAAGAGCCC 189

(2) INFORMATION FOR SEQ ID :1070:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1070:

35 TTTATTCCAC TGGAGAAAGG GGATTGAAAA TCAGTTAGAA CCAATGTATT 50
TCTTGCCCCA CGGAACACTA TTCCTATAAG ACAGCTGAAA GAAGCTGCCG 100
TGAGGAGCTC AGCTCCAAAC ACAGGATCAG CACCTCGCAT AGGAATTCCC 150
40 ATGAATCACG ACTTCTCATC CCGTTTTATC AGAGTGCATA TACGTCCTAC 200

543

TTAAGGAAAA GTAAACAGT CATTTACGAA AGAAAGTCAA TCTGTATCCT 250

AAGCATTTTA ATAAAAAGTC AGAAGGAATT 280

5 (2) INFORMATION FOR SEQ ID :1071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1071:

AGAACCGAAG CCTGCAGAGA GGCCATTCTG ACAGGCTGGG AAATGTAGCC 50

TACCGCCAGA AGCTAGAAGC AAGCACTTCC TCCTAACCGA GTTTTGTAAA 100

20 GACTAAGGGA AAGAGAATAG AGAAGGGATA TTCCCATCTA CCGGGGAAAA 150

GATGCGCAGT AACAAACCAT CTAGGAGAC AGCCTTCTAA CAG 193

25 (2) INFORMATION FOR SEQ ID :1072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1072:

AAAGCACCTT CCCCTCGCTG AGCTCCAGGG GGCCAGATA GGCCACGCGC 50

AGCTCCAGCA TCTTGGAGAG CTGCACGTCA TCTGCCGCGT CGTAATCCTC 100

40 CACTCTGCAG CCATAGGCCC CACTCTGGCC CCGGGTCACT CCCTCCAGGG 150

544

TCAAGTTCCC CTCGAGATTC ACATC

175

(2) INFORMATION FOR SEQ ID :1073:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1073:

15 AGTGCCCTAC TCTTTTCCCA AGAAGGGTCA AAGCCTACAA TATCATCAGG 50
GGGCATGAAG CACATTAATT TGCAGTGGCT GCTTCATATG AGGAGGTATG 100
GTGGACAGGC TAATTTTCC TTGAAAATGT GGCTTCTTCA ACTCCTTTCA 150
20 AATTAGGAT GGAATACTTC CTGAAATAAA AACTGGGCTT TATGCAGGAT 200
TCTCTTTGAA AATTCTTGTA TGTCCAGAAC AAAAGATAAA ACTAATTGTA 250
25 TTCCTCACAT TCACAATCCC CATTGGTCTG AAGTCACGTG ACACAGAGCA 300
TCTATATAGC ACATAGTGTT TAAAGACTAA TGAATGCAA 339

(2) INFORMATION FOR SEQ ID :1074:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1074:

40 ATTAATTATG CGGTCCTCCT CCTGGCAGCT GGACACCACT TTGAATCTTC 50

545

CTTTGAGCTC CGGAAAGTTG GTAATTACAA CTGATATTT CTACATGGAA 100
ATCAAGAAAC TCGGACCCAA CTGGTGCAA AGACGGATCT CCGCCGATTC 150
5 TGACGGCTCT CCAGGTTTTC TC 172

(2) INFORMATION FOR SEQ ID :1075:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1075:

AGAGTAGGAA GAGGGAGGGG AACAGGCATC TAAGATAGAC TTTCTCCATC 50
20 TGTGGGAGC CTGGCAAGT AGGAAGAAG CCTTTTTCAT AACTTCAGT 100
CGTATGACTG AGCTGCTTG CAGGGCACTG GAAACGACGA ACTCGCGCAG 150
25 CCTGCAAATG AGACCACTCT CATTCTCAG TTTCGATTG ATTCACTCAC 200
TAGTAGTTAG GTAAATACGA GCTCTATGTG ACTCAAGGAA TGTCAGGCTG 250
GGGCAGGTGG CAAAAGCTAC AGTGATCGAA ATTCACGTTG CTACTGATG 299

30

(2) INFORMATION FOR SEQ ID :1076:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1076:

546

	GCCCTCATCG GCGATACTGG AGGTTGCTT TCTCAACCCT GTGGGCTTCA	50
	CCCCAGACAC GCCCTGAATC GTTTCATGTT CCAGCATGCC TGAGACAATC	100
5	ATCGACTGAA GGATGTTCTC TAACACCCGC ACGAGCTGCC GGCAGATCTG	150
	AATGCCCAAG TCACTCAGCA CCTGCCGATA CTCAGCCAGG TCAAAATCGG	200
	CGAGGTAGTG CTCATGCCTG GCGAGACCTG TTGTGCTTAA TGAAGCCCTA	250
10	TCATTGGAAG TATTGCTATG AGCAGTGCGA AAA	283

(2) INFORMATION FOR SEQ ID :1077:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 297 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1077:

25	ACCAATCAAG TACTACTAAAT TAGAATATTT TTAAAGTATG TAACATTCCC	50
	AGTTTCAGCC ACAATTTAGC CAAGAATAAG ATAAAACTC GAATAAGAAG	100
	TAAGTAGCAT AAATCAGTAT TTAACCTAAA ATGACATATT AGAAACAGAA	150
30	GATATTACGT TATGCTCAGT AAATAATCAA GAGATGGCAT CGCGTAAGAA	200
	GGAGCCCTAG ACTGAAAGTC AAGACATCTG AATTTCAGGC TGGAAAATA	250
35	TCAGTATGAT CTAAGCCTCA GTTCTCTNGT CTGCAAATG AAAGCAC	297

(2) INFORMATION FOR SEQ ID :1078:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 291 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

547

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1078:

AATCTTTTAA TCAATCGAAA CCTTAATAAT TAGGACTGAT AATAGTGATC 50
AGTGATTGAA CCTTTATTAT TTACCAGCTA ATATAGTAGG CCCATAAATA 100
10 GGTTATATCA TTCGTAGTCA CAATAACCAC ATACATCACA CACCATGACG 150
TAGCGCTACT ACCCATACCT GCTAGCAGTC AAGGTTGAGA TAATCATAAC 200
15 ACGCCCAACA TCTCATTGAT AGTGAGTTAT CCAAACAGGA ACAATCTCAA 250
GTTTATATCT AAAGCCCATG TTCTTTTGCT TAATATTAGA G 291

20 (2) INFORMATION FOR SEQ ID :1079:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1079:

AGTCACAGCC CCTATACTCC CTCTACACAT TAACCACAAC ATAAGCGGGG 50
CTCACTCACC CACCACATTA ACACCACGAA ACGGGTAATC TAACACGAGA 100
35 AAACACCCTA ACGTTCATAC ACCCCATACA CCATTA 136

(2) INFORMATION FOR SEQ ID :1080:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

548

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1080:

CCAAGGTCGC CTGTGTGCTA GTCACGACCA TTAGGATCCG AAGAAGAGAT 50
GATGACTACC CTAAAAGTAA GGTCTGTGAA CAGCCTGTAA TGGGACGTGA 100
10 GCTGCGGTAT TAAAAAATC AAGAATGGAA GCGTTCCTCA ATTGTCGTTG 150
AGAATCATAC CAACACGGCA GATGCAACCA TGAAAAACGC AGCTGCGTAT 200
15 CGCGCGTTTT TCATGGTTCG CATCTGCCGT GTATGCAATG ATTCTCAACA 250
CACATTGGAG TCACGCGGCC TCGTAAGAG TATGAAGGTC TTCCTGTAAA 300

20 (2) INFORMATION FOR SEQ ID :1081:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1081:

GTTAATGGTT TTTTCATACA TATGAGACTG AGCGGTCAAA GTTTTACTAA 50
AGTCTTTATG ATCTTTAATT AATACTCCAA GACATCCGAG TTTGGCAGAT 100
35 ATTGGATGAG ATTTGTTTTG CTCCTTACTT TCTTGTATA CAGCCAAGCC 150
TGAAAATCTC TAGACATTTG CTGAAATTGA TGAGAGCATG CACAGGACGA 200
CTGAAGGTGC TGGACATGA 219

40

(2) INFORMATION FOR SEQ ID :1082:

549

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1082:

10

ATTTTGGGAA AGTGAGCATG AAGAAGGGAC TCAGAGCTGC CAGGTACCCG	50
AGTCTCAGGC TCTGACATCT CTTGGGGCCC CCTTCTGCCA CAACTTCTTG	100
CCACTTCACG GACTTGAATT ATGTCCCGCG CCTAAAAAAA AGATTGGCCT	150
GCAGCACAGG CGTGTATCCT CTCCAAAAAG CTGCTGCTCA TTTCTGGCCC	200
CATCTGCTGC TATCTTTGCC AGTCAGCCAT CACAGTTTGG CATCATCAGA	250
GTCTCAGCTA GAGGGAGCGT GTCATTCTG CCTTAGTGGT TTGCCTGCCA	300
CCTGACCAGG GCAAGACCAG CTGGGATGTC AAGTGACATT TTGGGAACTT	350
GTCGGAAGTT	360

25

(2) INFORMATION FOR SEQ ID :1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1083:

40

CATACATATG AGACTGAGCG GATCAAAGTT TTA CTACAAG TCTTTATGAT	50
CTTTCAATTA AATACTACTCC AAGACATCGA GTTTGGCAGA TATTGCGCCC	100

550

150
GCCGTTTTGC TCTTCTTATC TTTGTATCCA GCCAAGCCTG AAAAGTCTCT
200
AGACATTTGC TTGAAATTTG ATGAGAGCTT GCACAGGCCG ACTGAAGGAT
5
GCCGGACATG ATTCTCTGCT TTCTGGTTCA ACAAAAAA AAAGTTCCAG 250

(2) INFORMATION FOR SEQ ID :1084:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1084:

50
TNCTAGATAC NTCCCTCTGT CTCACATTCA TAGTGTGTTT TTGTCTAGTG
20
TATGAAGTCT CACNCAAGGA AAGTGTCAG GCAGAGTTTG GGGAGAGTGA 100
AAAAAGTGAA TGGCCTATAT NTGCTCTNTT GGGTGNTCCA NCCATTATTG 150
25
GGGTGAACCC TTTCAGCTTT TTCCTAAAAA TTTGAAAAGA NTTTTTTAA 200
AAATTAAAAA GAGGATTTTT AAAAGGAATA TCTTGTTCAA AATTNTTAA 250
GTTTAAATAG G 261

30

(2) INFORMATION FOR SEQ ID :1085:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1085:

551

	GCAATCCATA AGTGTCTTA TCTACAAAGT GAAAAGTTGG ACAAGATATT	50
	CTTCATGATC TTTTTCGATT TTAAATGTC ATGCAATTTT AGAGAAAAGC	100
5	TGAAGGGTCA CCCAATATGG CGCGACACCA AAAGACAAAT ACGAGGACAA	150
	TCACTTTTTC ACTTCCGCA AACTATGCCT GGACACTTCC TTGGCGAGAC	200
	TTAATACACC AGACAAGAAC AACTATGAA TCGGAGACAG AGGGAGACAG	250
10	AGGCGAAATA	260

(2) INFORMATION FOR SEQ ID :1086:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1086:

25	AAGACGTGGA TTTGCTGGAA GACACGGATT TCCTGGAAGA CCTGGATTTT	50
	TCGGAAGCTA TGGATTGAG GGAAGACAAG GATTTTCTGG AAGACATGGA	100
	TAATCTGGAA GACATGACTT TGTCGGAAGA CGTGGACTTG CCGGAAGACA	150
30	CGAATTCCT GGAAGACCCG GATTTTTCGG AAGCTATAGA TTTAAGGGAA	200
	GACAAGACGG ACT	213

35 (2) INFORMATION FOR SEQ ID :1087:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

552

(xi) SEQUENCE DESCRIPTION: SEQ ID :1087:

5 TCCCAGGCAC CCGCTGAATT TCTGAGGCCT TGCTTAAAGC TCAGAAGTGG 50
TTTAGGCATT TGGAAAATCT GGTTCACATC ATAAAGAACT TGATTGAAA 100
TGTTTTCTAT AGAAACAAGT GCTAAGTGTA CCATATTATA CTCGACGTCG 150
10 ATCATTTC TC AGTCCTATTT CTCAGTTCTA TTATTTGAGA ACCTAGTCAG 200
TTCTTTAAGA TTATAACTGG TCCTACATCA AAATAATAGA AATTACGTTT 250
TTTTTT 256
15

(2) INFORMATION FOR SEQ ID :1088:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1088:

TTGCTTAGAA CGGAGCTAGC AAGACAAAAA TACTTCAGTT GGCATCTCCC 50
30 TTAAAGCACA TCCCCAAACG CGGGTCCTGG CCCCAGACAG GGAGACCAGG 100
GCTCTGACAG TGACAGGTTT TTCCCTCTGA AAAAAGAATA GAAGAGGAGC 150
TCCTCCCTAA CCCACAGATT CCCAGGGCAG ACCCTGGGAG GAGGTGCTGA 200
35 AACACAGAAG AGAGTGTGTC TTCCCCAACC TCTACCAGAC AGTAGAGAAA 250
CTGAGGCGAG AGGC 264

40

(2) INFORMATION FOR SEQ ID :1089:

(i) SEQUENCE CHARACTERISTICS:

553

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1089:

10	GACCTGGAAT TTGTTTTCGT CTGTTTCAGTA GACTCCGATT TCAGAATATG	50
	TCGGAATTTT AGACTCCGGA ACTTTTGAGA ATGTCATTAC AGGAACTTTG	100
	TTTACATACC GAGCTGTTAG CCCAGTCAC TGGGTCCGAA ATTACGCCGA	150
15	TACCGAC	157

(2) INFORMATION FOR SEQ ID :1090:

- | | |
|----|-------------------------------|
| 20 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 366 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1090:

30	GCATATACCA AAAAAGGACA AACAGATAGA AGAGTCATCT CAGTGTGTAA	50
	CGAGGAAAAG ATTTATCTCC CATCCTCTGA TCCTCCATAT GATATCTGAT	100
	AGCGAAGATG ACAATAACCC CTTGACTCTT CACGAAAACG CGATGAGAGA	150
35	GAACTTGAA AAGTCAGAAA ATAAGTTCAT ACCGCAATTA ACCTTTTGGT	200
	CAAGTAATGG AACTTTTGA CTACTAGTGT AAGTCAAAAG ACAAAGGACT	250
40	CCAGCAAGAT GAGAGATTTC TCTATTTTGT AACGAGTAGT CCACCGATCG	300
	TCATCAAAGA GAGAGAATGA ACAACTACGA AAGTTTAAGG GAAAAAAAAA	350

554

AAAAAACATA GATGTT

366

(2) INFORMATION FOR SEQ ID :1091:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1091:

15 GGTCTGAATC ATGAAAAAGC CCATAAGAGA GATACAGTGA CTCCAGTTTC 50
AATCATATTA CAGGAGATGA ATCTGTTGCT CTCCCATTTT GCTCTTGTC A 100
CACCATATGA AGACATCAA AAACACTTAA GGATTCGAGA AAGAGAACAT 150
20 CTTTGTGTTAA AGAAGAGAAT AAGATTTTGG AAGAAAAAGT AATAGCAAAT 200
TTGAAGAAGA AACAAGTTAC GTAGGGACGA GAACAAGTAA ATAAGGCCTA 250
25 TCATGCATAT CGAGAGGTTT ACATTGATAG AGATAATTG AAGAGCAAAT 300
GGACA 305

(2) INFORMATION FOR SEQ ID :1092:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1092:

40

AAATGGAAGT TGAAGT GAGT GTGGTTTCCA GTACAGGGCA TCTGGCCACC

50

555

TTCACCTCAG TAAATACTGC TGATCGACTC TCTCTGGCTC TGGCTGTCCT 100
GCCAGAGACA GCCAAACACA GGAGACATGA CAAATTACTA TCATCTTTTG 150
5 CTTCTTTATT TTTATTATTA TTATTTTCT TTTGTGGAG AACAGCGTCT 200
TGCTGTATTG CCCAGCCTGA TCTCAAACCTC CTGGGCG 237

(2) INFORMATION FOR SEQ ID :1093:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1093:

20

AGAAATTTAT TGCCTCACAG TTCTGGAGCC TGAAGTGCA ATATCAAGGT 50
GGAGACAGGG TTGGTTTCCT CTGGAGGCCA TAATGAAAGC ATCTGTTCCA 100
25 GGTCTCTGTC CTTGGCTTGT AGAAACACGC ATTCTTCTGG TGGATCCACA 150
CAGTCTTCTC CATGTGTATC CTTCCCTCAG TTTCCCTTAT AGGACACCAG 200
TGATGTCAGA TTAGGGATCG AACCCAACAA CCTCATTGA AGTTACTCAC 250
30 CTGTTTGAAA ACCCTATGTC CAAATACAGT TATAGTGTA GGAAGTAGGA 300
CTTAGGGCTT ACAAATATGG AGTGGGGCAT CATCCAGACC ATACCATTTA 350
35 AATTGCAGGG TTTCTCTCCA ATGTGAGTTA CATACACACA TTAAGGTTTG 400
TGGGATTCAG AAAGGTATAC 420

(2) INFORMATION FOR SEQ ID :1094:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

556

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1094:

	GTTTCTTGGG TAACCTCCCC TCCTTAATCC TTCTGGCATA GGCAGACTCA	50
10	CAGCAGGTAC CCAGTAGAAG GTAAGGTGGC TGATCATTTT TCCATAGGAG	100
	GTCTCCATGG CACACAGGGT AGAAAGTGCA TTCTGTGAAT TAGAGGCAGC	150
15	AGAGCATGGC AGCTAATGGA AACTGGCTCT GGGAGGTCAA AT	192

(2) INFORMATION FOR SEQ ID :1095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1095:

	AGAGAGCTTA ATAAGACCTA ACTACAGGCA AACCTGACTG GAACGTGAGT	50
30	ATCTGTGGTC TGGTGTGGAA ATAGCTCTCT AGCCCCATCT CCCTCCTCCC	100
	ATTGTCCACC CCCATCCTCC TTACCACGAA ACACATTTTT CACCAGCATT	150
35	GCCAAACCAC TTGGGATTCC TGCGCATGGC TTTGCTTAGT TTGCTCTTCT	200
	GCTTCTTGGA TACCTCCTTC AGGAAATC	228

(2) INFORMATION FOR SEQ ID :1096:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs

557

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1096:

ATTTTTTATG GAAAAAGGGG GATAATGCAA AATAGCAAAA ATTGTAAACA 50

10 AAGTTAAAGA TTATCTTCAT CTAAACCTTA AGCTGACAAT TTA AACACC 100

TTGTGCATAA TGCAGAAAAA AACTGTCCGT TTGACTTCAC TTTCATTCAC 150

15 ACTGCTCCCT ACGCATGAGA AAGACCAGAT GTCTGGTTTC AGAGTATT 198

(2) INFORMATION FOR SEQ ID :1097:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1097:

TAGAGAGAAG TTGATATATG AAGATAGGGT GGACAGGACT GTGAAGGAGG 50

30 CTGAAGAAAA ACTGACTGAA GTGTCACAGT TTTTCTCTAC AAAACTGTGA 100

CACTTCAGTC AGTTTTTC 118

35

(2) INFORMATION FOR SEQ ID :1098:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

558

(xi) SEQUENCE DESCRIPTION: SEQ ID :1098:

5 AAAAGTCACT AAAGTCANTG TGTAATACGA AAACCGAACA CTCCAGCAGT 50
 CCTATTTTAT NTNTTCCAAC CTAGNNCACC CAGGTGACGC NNGGGACTCG 100
 TCNCAGGTGT TTNGNACTTG CCGCCCGACN GGCNAAGG 138

10 (2) INFORMATION FOR SEQ ID :1099:

(i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1099:

 ACTCCACCAC TGGGNCCGCC ATGTTTTGGG TNGGNGCAAT GCGCTGTCTG 50
 TGAGCGCCAN TCTAATTGTA TTNGGACTGC ACGGGTCCGT AACTGACTG 100
25 ACACTGGGCT ACCTCGCCCG AAAATGNGAA CACCGCTCAA TATCGNTGCG 150
 G 151

30 (2) INFORMATION FOR SEQ ID :1100:

(i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1100:

 TAGCAATAGG CTATAACATA AGCCGAGGTA TAGGCTACAC TAGCTAGGTT 50

559

CGTGTAAGTA CACTCTATAT TGGCACAACA TAAAATTAAC TAGTGACGCA 100
TTTCTCAGAA TGCATCCCCA TCGTTAAGTG ACACAGACTG TCCCTCATAT 150
5 CACCGGAGGA CTGGNCCAGG ACCTCCTGGC GGCACCAAAA TCCACGAGCG 200
C 201

(2) INFORMATION FOR SEQ ID :1101:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1101:

20

TAGCAATAGG CTATAACATA TACCGAGGTA TAGGCTACAC TAGCTAGGTT 50
CGTGTAAGTA CACTCTATAT TAGCACAACG ATAAAATTAA CTAGTGATGC 100
25 ATTTTTCAGA ATGCATCCCC ATCGTTAAGT GACACATGAC TGTCCCTCAG 150
TATCACTGGA GGACTGGGNC CAGGACCTGA CCTGGTGGTA CCAAATCCA 200
TGAGGCNGNA AT 212

30

(2) INFORMATION FOR SEQ ID :1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1102:

560

CGGTAGCAAT AGCTATAACA TATAGCCGAG GTATAGGCTA CACTAGCTAG 50
GTTCTGTAA GCACACTCTA TACNNGCACA ACATAAAATN AACTAGTGAT 100
5 GCATTTCTCA GAATGCATCC CCATCGTNAA GNGACACATG ACTGTCCCTC 150
AGTATTACTG NAGGACTGGN CCAGGACCTC CCTGGGGTAC CAAAATCCAN 200
GAGTGGAAAT TCCANCAT 218

10

(2) INFORMATION FOR SEQ ID :1103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1103:

GTAGCAATAG GCTATAACAT ATACCGAGGT ATAGGCTACA CTAGCTAGGT 50
25 TCGTGTAAGT AACTCTATA TTAGCACAAC GATAAAATTA ACTAGTGATG 100
CATTTTTCAG AATGCATCCC CATCGTTAAG TGACACATGA CTGTCCCTCA 150
GTATCACTGG AGGACTGGGN CCAGGACCTG ACCTGGTGGT ACCAAAATCC 200
30 ATGAGCG 207

(2) INFORMATION FOR SEQ ID :1104:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

561

(xi) SEQUENCE DESCRIPTION: SEQ ID :1104:

GGCGTCAAGT GGCCCAATCT AACAGCTCCA GGGTAGCCAC AACCATCGTG 50
5 ATGGATTGCC ATTATTGTGT GCTAGTGGCT AGAGGTAGAC CCAATAGAAC 100
TCTGCCCCAA CAGGGCAACA GCCAAGCTCA ATTCTCCAAG CCCCTGAAC 150
AGACCTTCCA CATCCAGGAG AAGCTGTTGT TGTCTAGAGC TACTTAGTGT 200
10 CAGAATCCAG GCCAGCTTGG CTGCTTGATG CGACTGGCTA TAGGATTNGN 250
GTGNAGGCC 259

15 (2) INFORMATION FOR SEQ ID :1105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1105:

ACATGACCCC TTGGACTGAA GCGCTCACT AGTAAAGGAG TGTCATGCAG 50
GTCAACACAT GTCGCACATG GACCACAAAG CCTGCCACCA GCAGGATGCA 100
30 CGGGGACTTC TGGGAGGGGG TGGACAGGAT ACTTATCTGT GACTGGAATG 150
CAGGCGAGAG GCGGAGAAGA GAGTGAAGGA TAACTCATAG AGGGGGCAGC 200
35 ATTTGTTTCG NGTTGAAAGA GGCAGAAAAT 230

(2) INFORMATION FOR SEQ ID :1106:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

562

(D) TOPOLOGY: lin ar

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1106:

ACATGNCCTG GACTGAAGGT GCTCAGTTAG TAAGGGAGTG TCATGCAGGT 50
CAACACACGT CGCACATGGA CCACAAATGC CTGCCACCAC AGGATGCACA 100
GGACTTTTGG GGGGAGTGGA CAGGTATTAT TGNGACTGGT GAGGTGAGAG 150
GTNAGAGGGG GCT 163

15 (2) INFORMATION FOR SEQ ID :1107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1107:

ACNTGATGAT TGCCATTATT GTGTGCTAGT GGCTAGAGGT AGACCCAATA 50
GAACTCTGCC CCAACAGGGC AACAGCCAAG CTCAATTCTC CAAGCCCCCT 100
GAACAGACCT TCCACATCCA GGAGAAGCTG TTGTTGTCTA GAGCTACTTA 150
GTGTCAAATC CAGGCCAGCT TGGCTGCTTG AT 182

35 (2) INFORMATION FOR SEQ ID :1108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

563

(xi) SEQUENCE DESCRIPTION: SEQ ID :1108:

5 CCCCCTGGACT GAAGGCGCTC AGTAGTAAAG AGTGTCTATGC AGGTCAACAC 50
 ATGTGCGACA TGGACCACAA AGCCTGCCAC CAGCAGGATG CACGGGGACT 100
 TCTGGGAGGG GAGTGGACAG GATACTATCT GTGACTGGAA TGCAGGCGAG 150
10 AGGCGGAGAA GAGAGTGAAG GATAACTCAT AGAGGGGGCA GCATTGTGTT 200
 CGNGCCTTGA AAGA 214

(2) INFORMATION FOR SEQ ID :1109:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1109:

25

 ACATGGCCCC TGGACTGAAG GTGCTCAGTT AGTAAGGGAG TGTCATGCAG 50
 GTCAACACAC GTCGCACATG GACCACAAAT GCCTGCCACC AGCAGGATGC 100
30 ACAGGACTTT TGGGGGGGGT GGACAGGTAT TAT 133

(2) INFORMATION FOR SEQ ID :1110:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1110:

564

GCATGACCCC ATGGCACTGA AGGTGCTCAG GTTAGTAAGG GAGTGTGATG 50
CAGGTCAACA CATGTCGCAC ATGGACCACA AATGCCTGCC ACCAGCAGGA 100
5 TGCACGGGGG ACTTCTGGGA GGAGAGTGCA TAGGATACTT GTCTGTGACT 150
GGAATG 156

(2) INFORMATION FOR SEQ ID :1111:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1111:

20

GGCGCTCANT GGATCCAATA CACCAGACTC CCGGGAGCGA AAACGCCCCG 50
AGGTGCCTCA AAGAACTTAA AACAGAACTG CCATTAGACC CCACAATCTC 100
25 ATNAAGGATG TTATAGATAT ATCCAAAAGA AAATAAATCA TTCTTCAAAA 150
AGACACATAC ACTAACACGT TCATGGAGCA CTATTCACAC AGCAAAGACT 200
CGATCAACTC ACACACTCAT GAATGCGGAT CGAAATAGAA GATGTGGTAT 250
30 GCATACACCA CGAAATACTA CGAGCCATAA AA 282

(2) INFORMATION FOR SEQ ID :1112:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

565

(xi) SEQUENCE DESCRIPTION: SEQ ID :1112:

TAATTAGTTT AACCACTGTG GAAAGCGTTG TAGGGTCTCA AAGACTNAAA 50
 5 ACAGAACTGC TTAGACCCCA CAATNTTANG AGCGGATGTT ATGATATATT 100
 CAAAAGGAAA TAAANNGNCN TGTNAAAGAC CATAACNAT NGTCCATCGG 150
 AGCCCGTATN CACGCAGCTT GTCATAACTA T 181

(2) INFORMATION FOR SEQ ID :1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1113:

ATCCAATGAC ACCAGACTCC CGGGAGCGAA ACGCCCGCAG GTGCTCAAAG 50
 25 AACTTAAAC AGAACTGCCA TTAGACCCCA CAATCTCATN AAGGATGTTA 100
 TAGATATATC CAAAAGAAAA TAAATCATTC TTCAAAAAGA CACATACACT 150
 AACACGTTCA TGGAGCACTA TTCACACAGC AAAGACTCGA TCAACTCACA 200
 30 CACTCATGAA TCGGATCGA AATAGAAGAT GTGGTATGCA TACACCACGA 250
 AATACTACGA GCCATAAAAG GCGAAATC 278

35

(2) INFORMATION FOR SEQ ID :1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

566

(xi) SEQUENCE DESCRIPTION: SEQ ID :1114:

ACCTGCAAAC TTTTCTGTA AAGACCAGAT AGTAAGTATT TTATGCTTTG 50
5 TGAGCCATAC AGTTTTTGTG GCAACTAGTC AACTCTCAAC TNACGTGGAC 100
AGCATGTAAA GAACGAGAGT GACTG 125

10 (2) INFORMATION FOR SEQ ID :1115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1115:

GTAGCGACCG GCGCTCATGG AATTCGGGA CCTGCAAAC TTTTGAAG 50
ACCAGATAGT AAGTATTTTA TGCTTTGTGA GCCATACAGT TTTTGTGCAA 100
25 CTAGTCAACT CTCACTCAC CGTGGACAGC ATGTAAATGG ATGGGAGTGG 150
CTGCCCG 157

30 (2) INFORMATION FOR SEQ ID :1116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1116:

CCTGCAAAC TTTTCTGTAA AGACCAGATA GTAAGTATTT TATGCTTTGT 50

567

GAGCCATACA GTTTTGTG CAACTAGTCA ACTCTCAACT NACGTGGACA 100
GCATGTAAAG AACGAGAGTG ACT 123

5 (2) INFORMATION FOR SEQ ID :1117:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1117:

ACCTGCAAAC TTTTTTGTG AAGACCAGAT AGTAAGTATT TTATGCTTG 50
TGAGCCATAC AGTTTTGTG CAACTAGTCA ACTCTCAACT CACCGTGGAC 100
20 AGCATGTAAA TGGATGGGAG TGGCT 125

(2) INFORMATION FOR SEQ ID :1118:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1118:

35 ACCTGCAAAC TTTTCTGTA AAGGACCAGA TAGTAAGTAT TTTATGCTTT 50
GTGAGCCATA CAGTTTTCGT TGCAACTAGT CAACTCTCAA CTTCACCGTG 100
GACAGCATGT AAATGGATGG GAGTG 125

40

(2) INFORMATION FOR SEQ ID :1119:

568

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1119:

10

ATTAAGCTTG ACACATCTGT GTTATCACGC ACTGAAGACA GGAAGCAGTT 50

CACTGAGTCA GCTGGCTTCC AAGCTTACAC AGAAGGCGAT AAGTCACTAT 100

15

CAAAGAGCCA ATGAGAATCT TCTTATAGAA TAACCTGGGC CCAAGTGA 148

(2) INFORMATION FOR SEQ ID :1120:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1120:

AGAATAACAG AGCCAAAGGA CTAATAAAAT CAATGAATCN TGGTGAGACT 50

30

AATCAAGAAA AAATAGCACC AACAACAATG AGGAGAAAAT GGAAAAAGGG 100

CAGAGTATTT CAAGGATTAC GAGAGGGCAA ACCAATCAAC GAATGATTCT 150

35

TAAGCCTTCA GTTTGCCCTG TAAGCAAACCT GAAGACGTGC AAGTCATCCT 200

TTGCCCTGGG AGAGTTAACT TAACCCACAG GGACAACTG 240

(2) INFORMATION FOR SEQ ID :1121:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs

569

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1121:

AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AAGAATCCTG 50
10 GTGAGACTAA TAAGAAAAAA TACACCAACA ACAATCCGAG AAAATGGAAA 100
AAGGGCAGAG TATTTAATGA TACGAAGATG GGCAAACCAA TCAATGAATG 150
15 ATTTTAAAGC CTTACGTCT GCCCTGTAAG CAAACTGAAG ACGTGCAAGT 200
CATCCTTCGG CCCTGGAGAG TTAACGTTNC CCAAGGGGCA ATGAGAAGGG 250
ACAG 254

20

(2) INFORMATION FOR SEQ ID :1122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1122:

AAACGAGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TCAATGAATC 50
35 NTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT GAGGAGAAAA 100
TGAAAAAGG GCAGAGTATT TCAATGATTA CGGAGAGGGC AAACCAATCA 150
ACGAATGATT CTTAAGCCTT CACGTTTGCC CTGTAAGCAA ACTGAAGACG 200
40 TGCAAGTCAT CCTTTGCCCT GGGAGAGTTA ACTTAACCCA CAGGGACAAC 250

570

GAG

253

(2) INFORMATION FOR SEQ ID :1123:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1123:

15 AAATGGGGAG AATCAACAGA GCCAAGGAC TAATAAAATT AATGAATCCT 50
GGTGAGACTA ATAAGAAAAA ATACACCAAC AACAAATCCGA GAAAATGGAA 100
AAAGGGCAGA GTATTTAATG ATACGAAGAT GGGCAAACCA ATCAATGAAT 150
20 GATTTTAAAG CCTTCACGTC TGCCCTGTAA GCAAACCTGAA GACGTGCAAG 200
TCATCCTTTG 210

25 (2) INFORMATION FOR SEQ ID :1124:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1124:

AAATGGGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TTAATGAATC 50
CTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT CAAGAGAAAA 100
40 TGGAAAAAGG GCAGAGTATT TAAATGATTA CGGAGACGGG CAAACCAATC 150

571

AACGAATGAT TCTTAAGCCT TCATGTTTGC CCTGTAAGCA AACTGAAGAC 200
GTGCAAGTCA TCCTTTGGAC CCTGGGAGAG T 231

5

(2) INFORMATION FOR SEQ ID :1125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1125:

AAGTCCCATC AGCAACCCGT TTTTACCAG ATGTCACTCA AGAATGCGCC 50
CGTGGCCCTC CAGTTCCTGC GCACTAAGAG CGTCCCGCT 89

20

(2) INFORMATION FOR SEQ ID :1126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1126:

AAGAAACCCG AGACMCCAAC TAATCCCAGA ACAGCTAAAA CCAATAAAGA 50
ACCAAAACTT CACGACCACT TTCCTGAGGA CCCTGCTGAG TGCTCATGAC 100
ACCAATACTG ACAATTGTAG CGGTAATACA TACAATGATT TAATAAGCCT 150
ATGCTACTGG ACACATGCCC ACACAATAAT ANTCANRTGT NTYGTTAGGC 200
CTACT 205

40

572

(2) INFORMATION FOR SEQ ID :1127:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1127:

GCAAGGCCTG GCCGACAACA CCCTTATTGC -TAAAGTAAAT AATGNCGCGC 50
15 GGGGCCTGGA CCACCCTCTG GAAGAAGATT GTACCTTGA GCTTCTCAAG 100
TCTGAGGATG AGGAAGCTCA GGCAGTGTAT TGGCGCTTTA GTATCACATA 150
A 151

20

(2) INFORMATION FOR SEQ ID :1128:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1128:

GAGCACCCCA GCCCATAACA CAGAACTCGT CCCCCTACCC CCCTCAGCAA 50
35 GCCGGAGAGG CTAGCCCAAG TAATCATAAY AACAGCCGCC CGAGAGCAGC 100
CCCAGTAGCA GCCCCATGGC CGGGCGGAAC ACCTACATCG ACAACCTCAT 150
GACAGACGAG ACCTGCCAGG ACGCAGCCAT TCGGGGCTGC AAGGCCTCRC 200
40 CCTTCGTCTG GGCCGCCGTC CCCGGAGAAA CGCTCGT 237

573

(2) INFORMATION FOR SEQ ID :1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1129:

GCCTCGTGGA AGTGACATAG CCTTTAAACC CTGCGTGGCA ATCCCTGACG 50
CACCACGTGA CGCCCAGGAA AGACAGGGCG ACCTGGAAGT CCAACTACTT 100
CCTTAAGATC ATCCAACATAT AGGATG 126

(2) INFORMATION FOR SEQ ID :1130:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1130:

30

GCCATCTTCT GTAACAAAAT AAATAGTGTC AAGCACTAAA TATATGCATG 50
AATGCATCAG CAATAAGATG ACAATCAAAG AATGCTGTGA AGATTGGCAT 100
CAAGATGTTA GCAGCATACT GCAGGACTAG GCTTAGAAGC CTACCTGCAG 150
TTTATTTGCA AGGATTTTTT TTTTCGRGGG GGAGGGGAGA GAAAAGTAAA 200
TGTGCTAACT TCGGATACTT GCCCTTATAA AGAATTCCTT YGTATC 246

40

(2) INFORMATION FOR SEQ ID :1131:

574

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1131:

10 CGAGGATCCG GGTACCATGG CAAGTCTCAT GAGGCTATTT ACCGAATTTA 50
TCCTCTGTCT GACCATGATT TTTCCCTCA AATACAACCA CTCCTCGACT 100
15 TTTCACCCTC AAAGTATAAA AAGTATGAAA NATAAACAAG CTCTTGCACT 150
GTACACTTAG AAGTGTAACA TTAAAGCATT ATAGAGCTAT CTACACACCG 200
ATAAATCCCA TCGAATCTTG AATAATCCAT CAATACGTAG AACGCAAGGG 250
20 TGCAGACAGA ACTAAAACCA ACT 273

(2) INFORMATION FOR SEQ ID :1132:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1132:

35 GAGGATCCGG GTACCATGGT CTGTATATCT GTGCTTCCAC TTCTCGGAGG 50
TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG AGAATCCTAT TCAGTGCTCC 100
CTTAGACATT CTTCCAGGCA GGATCAAACCT CAAAGGAAAA GGAATTTGTG 150
40 AAGCAAACCA TGGCTTTGTC ACAGTAAAGT AATTGTCACT CTCACCCAG 200

575

AATGTGTGAA GCGCTGCAGG GAGAAGCTTC TCTTCCAGGA GAGCAATANA 250

AGCCAATGTA TCTGACCCCTT GCTTYGATGA GAGTTAATAA TAAGTATTAT 300

5 ATTTCTGTTT GTTAAAAAGT TCAGAATTT 329

(2) INFORMATION FOR SEQ ID :1133:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1133:

CCCCGAGCTA GTTGTCCCGA CCTG 24

20

(2) INFORMATION FOR SEQ ID :1134:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1134:

GAGGATCCAC AAACCATGGA ACACTCTCGC GGCTGCCACT CCCCCATGAC 50

35 CACCCTACAG GCCCTAACCC CAGCCCCTCA CGTTATCGTC CAGCCACAAA 100

TAGCTGCCGC CCTGAGATCT CCACCTCAGA CCCTCTCCCG AAGCCCACAG 150

CGGCCCCCTGC CGGGCACCCC AGCTTCCTCG CAGGCACCAA AAGCGCAGTT 200

40

CCAGGAATCT CTACCCTAGA GTGATCCGGC GCCAGTTGCC AGTTAAGGGA 250

576

CCAAACCTCG CCAGAAGGCT TCTTTTCGGG TTGATCGCCA TCTATTY

297

(2) INFORMATION FOR SEQ ID :1135:

5

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1135:

15

GCCGCTTTAC TGCTCAGTTC GGAGCTACCG CTCGAAAGC AACAAAAAAG

50

CNTTTGCAAA TGAAACGAGA TTGCTGAATT GCGTACACCG AGA

93

(2) INFORMATION FOR SEQ ID :1136:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1136:

30

CGAGGATCCG GGTACCATGG AGCTTCACAC GGGTCTTCTT GGTCTCAGGG

50

TTGTGGGAGA TAACGGTGGC ATAGTTCCTT GATGCCCCGG CCAGCTTGCC

100

35

ACGGTCTCCA GGCTTCTCCT CCAGGCAGCA CACGATTGTA CCCTCAGGCA

150

TGGTGCCAC AGGGAGCRCA TTGCCAATGT TGAGCTGGGC CTTCTTGCCG

200

CAATACACAA ACTGGCCCGT GNGAATGCCC TCGCGGGCAA TGAACAGTTC

250

40

CGCCCCGCTTC TTAAACCAAG ACAGATCCCG GAAGGCCGCC TGGGCAAGGG

300

577

GCCCCTCRAA CCCGGGGCTA TACACGTCAA AATC

334

(2) INFORMATION FOR SEQ ID :1137:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1137:

15 CGAGGATCCG CATACCATGG CCCCCATCTT ACGAGCCCTT ACTCCTCATG 50
ATGAAGAAAC TCCAAACCCT TTGACAGCTC CTCGGGGTNA AACCTGGNAY 100
AAAGCTGACT GACCAGGCTC CATGAAATCT CCCATCTCCA TRATGTACCT 150
20 CCTTGRTGCC ATCTCTATAT AAAGMGAACC AGTCCTAAAA TCAAACACT 199

(2) INFORMATION FOR SEQ ID :1138:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1138:

35 CGAGGATCCA AATACCATGG CGTCCCTCC TCCCGAGCGC CGTCCGCGT 50
GGCACCCGGC TCGTCCGAG TTCAGGCTC GTGCTAAGCT AGCGCCGTCG 100
TCGTCTCCCT TCAGTCGCCA TCATGATTAT CTACCGGGAC CTCATCAGCC 150
40 ACGATGAGAT GTTCTCCAAC ATCTACAAGA TCCGGGAGAT CGCGGACGGG 200

578

TTGTGCCTGG AGGTGAAGGG GAAGATGATC AGTAGGACAG AAGGTAACAT 250

TGMTGACTTG CTCATTGGTG GAAATGCTTC CTCTGAAGGC CCCGAGGAAG 300

5 AAGG 304

(2) INFORMATION FOR SEQ ID :1139:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1139:

GAGGATCCGG GTACCATGAG AAACCTTTGAA GCCAGAGATT TTAAACAATC 50

20 AAGGCACTTG AAAACATTAA GTATATGTAC AAATGTGCAA GTAAAACAAA 100

CAGCTGTACC AACGAGTAAC AAAGAAACAG TAAATCTTCA TCTTAACAAC 150

25 CTTTAATAGT TATCTAAATG CAGAGTTTGT TTATGAAATG AACCAAAGCA 200

GTTTGTCAAT TCTTACTATA AAATACCGAA AATAAAGTGC AAAACTTAGC 250

CACTACTGGC TAAAGAAACT AAGTAAA 277

30

(2) INFORMATION FOR SEQ ID :1140:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1140:

579

CGAGATCCGG GTACCATGGC CTCCTACAGG TGCCGTGGAG CCACGCCCAA 50
AAGAGAGCTC CCTGAGAAAC TCGTTGATGC CTTGCTCACT GAAGGAGCCT 100
TTAGCAGAG CAAATTTTCAT CTTGCGTGCA TTGATGGCGG CCATGGCGGG 150
GTACCCAAAC CCTCCAATTC CCAACGCGGT CTCAAGTTCA GACTGGGCTC 200
CAGCTTCT 208

10

(2) INFORMATION FOR SEQ ID :1141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1141:

CGAGGATCCG AGTACCATGG CCTCGAACTG AGCATCAATA TATTCTACTG 50
CCAGCTTATA ACTGTCATCT TTATTCATAT GGTCTCCAAA TCCCACGATG 100
TCAACAATGG TTAACCTCAG CCGTACATTG CTTTCCTGAA GCTCATAACT 150
TCTGGCTTTT AACCGAACAC CTGGTTCATT GTGAGTAGCT GGGTCACTTT 200
TAAATTTGGT GTTGAACAAA GTGTCCATTA ACGTGGATTT GCCAATGCCT 250
GTCTCACCAA TACAAAGGAT GTTG 274

30

35

(2) INFORMATION FOR SEQ ID :1142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

580

(xi) SEQUENCE DESCRIPTION: SEQ ID :1142:

5 GCCTGCACAT TGACTGTGGG AAACTCGGAA ACAAGCTCAC ATCTCCCGT 50
GGGAAACCTT CTAGCAACAG GATGAGTCTG CAGTGAAGT GAGTTGCCAC 100
CTTCCTCTAT GCGGAGGTCT TTGTTGTGTT GCTTCTCTGC ATTCCCTTCA 150
10 TTTCTCCTAA AAGATGGCAG AAGATTTTAA AGTCCCGGCT GATGGAGTTG 200
TTAGTGTCTT ATGGTAACAC CTTCTT 226

(2) INFORMATION FOR SEQ ID :1143:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1143:

25

RGGR TCCRNG TGCCRTGGGG YNTNNCTAGR CRGCRGGYAA GGTCCACCRC 50
TGRRCRCGNTG NCNGTGAGGR CRTGNRGGNC CRTGCGAGTG GGCTTACCGN 100
30 TAGGTTTCGGG AATGACCTTG CYMACGNCNN YGACAGCTAA GTRGRNGCRG 150
GNANGRTGNN GTGGAGRG 168

(2) INFORMATION FOR SEQ ID :1144:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

581

(xi) SEQUENCE DESCRIPTION: SEQ ID :1144:

CGAGGATCCA AATACCATGG AGCTGACAAT GTCAGCTCAA TTTGAAGTAT 50
5 TCTTGAGGGA CCTTTTGCTC ATAGGCTTTA ATTCTGTCTG TGACTTTTGC 100
CAGGATTTGA GGAAATCGAC TGCCTTCACT CTCCTTGAA ACTTTGAAGT 150
CCACATAAGG GCTTTCTCAT CAAATGGCAG AAATTATAAT TTATAAACCT 200
10 AAACAACCTT ATAGTGTTTT CGCTTTGAAT TGTATGAATT CTTAGAACTG 250
AGAAGT 256

15 (2) INFORMATION FOR SEQ ID :1145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1145:

AAACACAAGG CTAAAGTCA CTAAAGGTGA CACAGTACCA ACCCCGGGAA 50
GGTTGAGTTC TGTGCTGCTA CCTTCTACTG ATGGCGAATA GACTATTCTG 100
30 TACCCTGTGA TGGGAGCCTG GGGTCTGCTC CAGCAAACAA CAATCGAGGT 150
GTAATCAACT TGGTCCACAG TCGGGTCAGG AGGG 184

35 (2) INFORMATION FOR SEQ ID :1146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

582

(xi) SEQUENCE DESCRIPTION: SEQ ID :1146:

5 CGAGGATCCG GGTACCATGG CCCAAAGAGT GAATGATGTA TCCCAGGGCG 50
CAGTCCACAA CTTGCGCAGT ACCTTCCCAG ATGACAGCCT CACTGGACCG 100
ATTTCCATCC ACGAAGATGA TGCTAAGAAG CACCATGAGC AGACCCAGCT 150
10 TGGGTGAGTC CTTAGTCGTT CCCAGTATGC CTGCATCAGT GGGCTCTAAG 200
GTGCTGAGAA GAATGCACAA G 221

(2) INFORMATION FOR SEQ ID :1147:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1147:

25

CGAGGATCCA AATACCATGG GAGTCAAGCA TGCCTCGATA GCCACAGATT 50
TACAAGAATT ACCTACAGTT TGCTTCTTNG AATCGACATG CAAATCTGCT 100
30 TAAGGATTCT CACATTCAGG ACAGAGAACA AATTTTTTAA TGAATCCATC 150
CAACAGGTCT TGNAGTTTAT TCGCCTCATG AGATCCATTG ATAATGGAAC 200
RRTMATTCTT AACANCAAAC NGMGMTGNN NTCCCRNCTT ATAACCMAAA 250
35 GATNT 255

(2) INFORMATION FOR SEQ ID :1148:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid

583

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1148:

	CGAGGATCCA GGTACCATGG ACGATTACACA GCCCCTGGCC ACTGGCCATT	50
10	TCCAGTGGTA GGGAGCACAC TGRTACATT CGAGACCCAC CACGTTGAGC	100
	AGACAAAGGC AGCCTCCACT CTCCTCGTCA CTCAACATGT ACCTCCGTCC	150
	CCCAGGATGT TGTAAGTTATA GCAATAGCAG CCCTGCGGTT GACGTAGGTG	200
15	AGTCGGTGAC GCCCGATTG GATCGGGTGT	230

(2) INFORMATION FOR SEQ ID :1149:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1149:

30	GTGCCGTTGG TCCTGTGCGG TCACTTAACC AAGATGCCTG AGGAAACCCA	50
	GACCCAAGAC CAACCAATGG AGGAGGAGGA GGTGAGACG TTCTCCTTTC	100
	AGGCAGAAAT CGCCAGTTG ATGTCATTGA TCATCAATAT TACCNACTAG	150
35	AACAAAGAGA TCTTCTGAG AGAGCTTATT CAAAATACAT TAAATGTATT	200
	GGACAAAATT CGATATAAAA GCT	223

40

(2) INFORMATION FOR SEQ ID :1150:

(i) SEQUENCE CHARACTERISTICS:

584

- (A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1150:

10	CGAGGATCCG AGCACCATGG AGAGACTATG ACGCTCAACA AGAATCACTC	50
	GGAGGGCGAC GGAGTGATCG TCAATAACAC CGAGATTC CTAATGCCCT	100
	ATGATCACGT GGAACATAACA TCAATGACA TGAAGAACGT GCCAGAAGCC	150
15	TTCAAAGAGA CCAAGAAAGG CGCTGTCTAC CTTACTTCTC ATTGAACCAT	200
	CTTTATGTCC AAGAACAAGG ATGCGATGGG TATTTCTGTA NGCTATTTGA	250
20	NMTRAGGRMA GNCTGNAAGG TM	272

(2) INFORMATION FOR SEQ ID :1151:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1151:

35	TGAGGATTTA TAGATTANAG CTAGAGTTCA CATTTTATGG ATTACAACCA	50
	AAAAAACCT GAAAAAGAAA AAAACAAAAA AAGCTCAAAA GCAATCACAA	100
	GGATAGTTGA ATCCCTCTTT AAACCCCAAA AGCAACCCCC	140

40

(2) INFORMATION FOR SEQ ID :1152:

(i) SEQUENCE CHARACTERISTICS:

585

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: doubl
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1152:

10	AAGGATCCGG GTACCATGTA TTCCCCGGT ATCAGCAGAG GCGTGACGG	50
	GCACTGCTTT AAAACTGGGA AGGAGGAAGA CGAGGCCAGG GAGCCGGAGG	100
	GTCACCAAGG TAGATTTCCA GCAGCCTAGT CCAGCTGAAC GCTTCCAGC	150
15	CTTGCTTTTT AGCAGCTTTG AGGAAAAGTA TAGTGATCCG GATGTGAAAC	200
	TTTCATTG	208

(2) INFORMATION FOR SEQ ID :1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1153:

30	CGAGGATCCA GGTACCATGG GGTGGATCCG CCGGGCATAG CCACCCTGGA	50
	TGGTGGCCAT GGTGAGGCCG ATGAGGAAAA ACATCTTCCC CTGCTGTAGG	100
35	CTACTGAACT GGAAGCGCTG GTGTGTGAGG AAGCTCAACG TGCACTCCAG	150
	GCCCAAGAAC AGGAAGAGGT AGAGGAAGTA GACTMGGCCC AGGCGGCCAG	200
40	GCTGATGAAT TGTCTCCAAA GGGTGAGACC TGGCCACGAG CCATANCCCCA	250
	GAMGCCNMAC AGGGCTRGGG ACTG	274

586

(2) INFORMATION FOR SEQ ID :1154:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1154:

GAGGATCCAC CGACCATGGA ACACTCTCAA TGGCTGCAAC CACCCCGTGG 50
15 CCCCCCTACC AGCCCCAATC TCCAAACCCC GCACGTCGAT CATGACGCCA 100
CCAACAGCTG CAGCCCCTGA GATCTTCACC TTAGACCCTC TCCCGAAGCC 150
CGCAGCCGCC CCTGCGAACC CTCCAACCTG TTCACACGCG CCGAAAGCCT 200
20 ATTCCCAGGA CTCTCTGCCC CTACGTGACC GNCCCTAGCT GCTAGTCGAG 250
AATCCGAACT CCGCTCC 267

25

(2) INFORMATION FOR SEQ ID :1155:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1155:

CTCAAACCCC GNTTCCCCC TAATAAGAGC AACTAAAAA CTTCTGATAA 50
CCACAATAAA AGCGTGCATT TGAGCACAAT TCAAAAGCCA ACCCCTTCGA 100
40 AGGNGCTTCT GATGNAAAAG GAGTTATGTT GAACGAAGCA GGAGTTAACG 150

587

CTACACAGTC AAATTGTGGC ATTAGGACGC GCGAGCGGGC TAGCTGCGGC 200
CGTCTANCAA GGCAACGGCC GCCTTTGAAT T 231

5 (2) INFORMATION FOR SEQ ID :1156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1156:

GCGCGAGCAC AGAGCCTCGC CTTTGCCGAT CCGCCGCCCA TCCACACCTG 50
CCGCCAGCTC ACCGTGTATG ATGATATCAC CNCGCTCGCC ACCAACRACG 100
20 GCTCYAACMT GTGCAAGGCC GCCTTCAA 128

(2) INFORMATION FOR SEQ ID :1157:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1157:

35 GCCGCAACAC AACCCAGGGA GACTCAAGNC CACAGGGGCC CCCC GGCTCT 50
GAGGGATTCA CCGTCGCCTC CCGGTCCCCG AAGGCCCA CA AGGGCAGAAA 100
GGTGAGCCTT ATGCACTGCC TAAAGA 126

40

(2) INFORMATION FOR SEQ ID :1158:

588

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1158:

10

AATAACCATA ACTGCAAAAA CCCAAMCAAA AAAAAAGGGG GAACAAAAAA 50

CCCCAAACCC CCAAAAAAAC CAGAAAAAAC CACAAAAAAA AACCCCTCCT 100

15

T 101

(2) INFORMATION FOR SEQ ID :1159:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1159:

GAGGATCCGG GTACGGGCAG GGTGAGAGCC TGGGGTCCAC CGATAACCGG 50

30

GAGGGAGATG GCGTTCTTGA GCAGAGGGGA TGGGCCGTCC GGGAGCTCCC 100

CCCACACACG GTGGCGGTGC GGGTGAAGTGA GAAGGGGAGG TCGAAGGTGC 150

35

CATCTTCTTC AGGCCCTCC AC 172

(2) INFORMATION FOR SEQ ID :1160:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

589

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1160:

GAGGATCCAC ATACCATGGA ACAGCACCAC AAAAATAGCC ATTTTGATCA 50
TGGTTATTTT CCAGGACCAC ACGATTGTC TACGTCAC TG GAAGGCTATG 100
10 TGTCTGTTCT GAGCCTTCCC ACTCTCCTAA AGGGCAGATG AAGATCAGAG 150
CTTTGACCCT GTGATGCCAT TTTAATCAAC CCTGCTTGGT TTTAGAGGAT 200
15 TGCTCCCGTG GGTCACCTGA GGCAGGCTCC ACCTT 235

(2) INFORMATION FOR SEQ ID :1161:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1161:

GAGGATCCAC CAACCATAGA AAGTAAATAC TGTATAAAAA GCTCCAGCTG 50
30 TTAGATACAA ATGCAAAACG CTCCTAAAA AACGGCCTGA AAAAAAAGTC 100
ACAGACAATG CCAAACCTTA TAGGTCTGTA TTTTCCTTTA TACAAAATGC 150
35 CCTCAAATTA AAAAGTAATT CCCATATAGC AATAAAGTCC ACATCTCTGG 200
ATTACCTATA ACCGGTATTA TGGGGTGTGT TTATACTGCC TAGAATGTTA 250
ACCCTCATAA AGCCTTAAAA GTACATTTGT GAAA 284

40

(2) INFORMATION FOR SEQ ID :1162:

590

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1162:

10

GCTCACATAA ATTTCTTCAC CGACCCTTTT CTTCCAGCT TCCTTACTAT 50

AAAAAACCCC ACA AATA TGTTCATCAT CATCCATACT AACCAACCCC 100

15

GTCACCATCT CAATCAGCAG CAAGTCCTAC TCTCTGTGGG TGAAACCTTG 150

TTACCACCTC TAGGGGCAGA CCCCTTTTCA GATATATTCA AGAGTTTAAT 200

ATCCTCCAC TATAGCGCTT CGACTTTGTA TCTTCCTCTA TGGCTACCAA 250

20

ATTCTGTCCG TTGATAAGTA CTGGCTCTAA ACCATGC 287

(2) INFORMATION FOR SEQ ID :1163:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1163:

35

GAGGATCCAA AAACCATAAA ATTCATCATC CCCAGCAGGT GCNCTAGCTA 50

TACTTTATTA CAGCAAARCA CAACCACACG CTGAMCTANM TCGTATAGAT 100

AAACACCAAT CATGGGTCGG CC 122

40

(2) INFORMATION FOR SEQ ID :1164:

591

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1164:

10

GCGCGGGTCT GTCTCTTGCT TCAACAGTGT TTGGACGGAA CAGATCCGGG 50

GACTCTCTTC CAGCCTCCGA CCGCCCTCCG ATTNCCTCTC CACTTGCAAC 100

15

CTCCAAGACC ATCTTCTCGG CCATCTCCTG CTTCTGAAGC CT 142

(2) INFORMATION FOR SEQ ID :1165:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 219 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1165:

30

TATTCCTCCG GTATCAGCAG AGGCGTGTAC GGGCACTGCT TTAAACTGG 50

GAAGGAGGAA GACGAGGCCA GGGAGCCGGA GGGTCACCAA GGTAGATTTC 100

CAGCAGCCCT AGTCCAGCTG AACACTTTCC AGCCTTGCTT TTCAGCAGCT 150

35

TTGAGGAAAA GTATAGTGAT CCGTATGTGA AATTTTCATC GCACGTAGCG 200

GATGAGAATA GAGAACTCA 219

(2) INFORMATION FOR SEQ ID :1166:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 base pairs

592

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1166:

GAGGATCCAC CAACCATAGA AAGGAAACAA CACTTGGAGT GAACCCGACC 50
10 CAAGCCACTA CACCCCAGCC TAACCGACAG GTGCTAGACT AATNGTNAAA 100
AACAACCGGA AAATAGACCC GGACGAAGAT CAAAGNTTNT CAATCCAAAC 150
15 ATTTTAGGGG GACCAAGACC CMGGGATCAA AAACAAGGTC CACCACACCC 200
AA 202

(2) INFORMATION FOR SEQ ID :1167:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1167:

30

GAGAAACCTA CCCAACCAAG AGGCGCCCTG CTTTGTAAATG ACCTTTACGA 50
AGACACGTCT GATACCCAAC CTGACAGAGG AAACAACAGT AGTCTGAAAG 100
35 GGACAGAATG AGAGAGGGGG CTGGAGAAAG AAATGAATAA ACATGAATGC 150
ATCTGGAGA 159

(2) INFORMATION FOR SEQ ID :1168:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs

593

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1168:

CCCTAGACAA GCCACCTGAG GAGAGGCTCG GAGCCGGGCC CGGACCCCGG 50
10 CGATTGCCAC CGCTTCTCTC TAGTCTCAGC AGGGGTTTCC CGCCTCGCAC 100
CCCCACCTCT GGACTTGCCT TTCCTTCTCT TCTCCGCGTG TGGAGGGAGC 150
15 CAGCGCTTAG GTCGGAGCGA GCCTGGGGCC ACCGCCGTGA AGACATCGCG 200
GGGACCGATT C 211

20

(2) INFORMATION FOR SEQ ID :1169:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1169:

30

GGATTTCCGG TCCTGGCTTT CTGATATTTC TAAAATCGAC CTGGAATCAA 50
CCATTGACAT GTCCTGTGCT AAATATGAAT TCACTGATGC CCTGCTGTGC 100
35 CATGATGATG AGCTGGAAGG GCGCCGGATT GCCTTCATCC TGTACCTGGT 150
TCCTCCCTGG GACAGGAGCA TGGGTGGTAC CCTGGACCTG TACAGCATTG 200
ATGAACACTT T 211

40

(2) INFORMATION FOR SEQ ID :1170:

594

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1170:

10	GAGGATCCGC GCAACCATAG AACTCACAAC CCAGCCATAT ACCTCAGACA	50
	CAATGGAATG GCGGAGGTC GAGGTNGACA AACCTGAGT AATGTTGGGC	100
15	ACTTCCGCAC CGGAGCTGTT CTTACCTTTG ATAAAGTGA TGTTATTGCT	150
	ATTAATGATC TCTTAACGGA CTTCAACTGT AAAATTNGCA TGATCTAGTC	200
	CTATCCACCA ACGNCGAACA ATATGCTGTT GCCAMGATTG AGCACGAGCC	250
20	GTTTGGGCTC AACGGC	266

(2) INFORMATION FOR SEQ ID :1171:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1171:

35	GGCACAACCC ACTTTGAACA ATCATGCTTC AGAAATCTGC CTGACCTTAG	50
	CTGCTGCTGC TGCTCACTTT ATTATAGTAT AACTTCGGTA GGCATACTTG	100
	GAGAACATAT CCCACATTAG GAATTGATTT AAGCCTGAGA GTTTGAGGGC	150
40	TTTAATCCTT TAAACT	167

595

(2) INFORMATION FOR SEQ ID :1172:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1172:

AATAAACCTC CCTATCACAG TGACCTACTA CCCGCGTGTG CTTATATAAC 50
TAATCCAGGA CAACCCACAA AAATTATAGC AACACACAAA CACACCGCTG 100
ACCATAACAT GTGCGTCTTT CAAAGATGCC TTATCAACCA GAGCGATGAT 150
TACTGAGGAT ACGCAACTCA TAAAACTCTA CTAAAGCAA CAGGGCAGAC 200
GTGCGTCTGT GCCAGTCGTG AATGTGGTGA AC 232

(2) INFORMATION FOR SEQ ID :1173:

25

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1173:

GAGGATCCAC CAACCATAGC CCGAAAATGT GGTAAGGGAC CCTCATCTAT 50
CACACAACNC AGGTAAGAAG GCACCCAGCC CCATGGGCCA TAC 93

(2) INFORMATION FOR SEQ ID :1174:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs

596

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1174:

GCCTTTTTTT ACCCGCCGGA AGCTACAGCT TTTGCCCCCC CAAAAAACC 50
10 CCACCCTTTT ACCCACC GCG GACCCAAAAA CAGCAAAAAC CAAGGACCTC 100
TCCCAACCCC AACCCCTCCT TTTTGGCCCT TCCTTCCCCC CCTCCCAGCC 150
15 CACCCCCAGA CACCTCAATC CCCCAAAAGG ATGCCCTAAA CCTCTCCTAA 200

(2) INFORMATION FOR SEQ ID :1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1175:

GAGGATCCAA AAACCATGGC ATTCATCAG CCCAGCAGGT GTCCCAGCCA 50
30 TGACTIONACCA TAGCAAAACA CAACCACACA CTAACCTGCA TCGCCTAGCT 100
TACTGATGAT GATGTCCTGG T 121

(2) INFORMATION FOR SEQ ID :1176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

597

(xi) SEQUENCE DESCRIPTION: SEQ ID :1176:

AACCAGACAC GCCGACCCGC TGAATC

26

5

(2) INFORMATION FOR SEQ ID :1177:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 178 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1177:

GAATCGATCT TGACCTGGCT GCCAGGAATA TCCAGCTTGT TACCGACTGG

50

20

TAAAGAATAA GACCGCTGAT CATAGAGTGA AGCTCCAGGA ATCAGAGAGT

100

CTCATAGCAA ACCTCGAAAC TGAGGATGAG ATGATTACAG ATAAAGCCTT

150

TCAGGATGGA TTMAAGNAMG CAGAGAGG

178

25

(2) INFORMATION FOR SEQ ID :1178:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 144 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1178:

GGTTAAGTTT TTCATCAAAG ACTCAGGTAC CTATTATCGT TCCCTGGCGA

50

40

AACTGAGGAG AAAAGTTAAT CAACCAGGTT ACTCCCACAG TTGCCCCGTG

100

TGTTATGCAT CAGTTATACA GGTATCCCAC CAGTTCAAG TCAA

144

598

(2) INFORMATION FOR SEQ ID :1179:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1179:

GACCAGGGAG GAGGTTTAAT CAACTTGGAC CCCCTCCGGC CTAGCCGCCC 50
15 AGGAGGTGCA TTCGGGACAA CCACTAGGTC AGAACGCAGC CTCTCCAGAG 100
TCCTCAGGCT CGACAACGAT TATCCTGCTG CTATCACGCT TTGATTTACT 150
GATCTCGCTG AAAAGACAGA CGCTTTTAGA TACCGAGTCG ATAGGGGGTC 200
20 TCGGGTACTT TTCAGTAGAT AGGTGGTGCT TGT 233

(2) INFORMATION FOR SEQ ID :1180:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1180:

CGAGGATCCG GGTACCATGG GCCGGATACA ACGAGCTATC ATTACTGCTC 50
35 CCATGGCCAA AACCAGCAGT CCCACAATCC CCGTGAAAGG GATGAGGTAA 100
TAGCCCAAGG GGAAGGTATT GTCTGGAACC AGAAGCGCCC GAGCCCCCTT 150
40 CTTGTAGRCA AAGAGGGCGC CCAGGTGCTT GGAGCTNCTN TCCCCAATGG 200

599

AGGTAGACGG GACCAAGATC TGCTG

225

(2) INFORMATION FOR SEQ ID :1181:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1181:

15 TGAGGATTTA AAAATTCTGG AATATCTATG ATTGATCGTC AACTTTATTC 50
GATGAATAAG CTTGATGTGG CCTAGTTTTN NGNNNNNTGG NYATGGTNNA 100
TCNNNTTANT TTTTGTTG TTGTGNATAT TATNGAATAR AMGAATRGNG 150
20 TTTAGAGTTT GGAAGCGGCN RNGCGTARMG NNACTCYACG CTCGCNNCTN 200
TTGNNNNACA GMRGGNTCTC TNGGRTGAGT GGRINCMGTT GGMGGNNTCN 250
25 NNNTAGCTGN NGNGAGRATC AGCTRGCTTN CTTGNGCTN GCT 293

(2) INFORMATION FOR SEQ ID :1182:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1182:

40 GAGGATCCGG GTACCATGGC TCTCTCTTTC TTTTCTTCT TTTCTTGGC 50
GGATGTGAGA GCTGCCTGAG ATTCAAGGTC ATCCGGCAGC TCAGTCCCCA 100

600

CCACCTCTGT CTCTGGCTCC ACTGTGGCAT CTTGCTGTTT TTCTTTCTCA 150
GTCTTCTCTT AGGGAGCTGC CAGAGCTGCC TGGACCTGAG AATTCATTCC 200
5 TTCTGGCTGT TGAGACCCCG TGGACTCCCC TGGATTCCAG AGNNTNATTT 250
NG 252

(2) INFORMATION FOR SEQ ID :1183:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1183:

20

ACGAGGATCT GAATACTCTG GCCTGCAAGT AGAGGCTAAT TCGATGTGTG 50
AAACTGTAGA TTCGGCTTAA GGTAATAGTC ATTTATAGAC TATTCAATAG 100
25 AGTCAGACTG GTCGAGGCTG GTAAGTGTAG CGGAACGGTT GCTGACTGAT 150
ATTGTTAGAG TGAGGCTTGT ACTGGTGTGT ATCCGTAGGT GGTCTGCAGT 200
GT 202

30

(2) INFORMATION FOR SEQ ID :1184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1184:

601

CAGATCCTCA GCTTTCGTGG TTCACAATTT CTCAGTCTC TTA

43

(2) INFORMATION FOR SEQ ID :1185:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1185:

15

ACCGTCCTTC TGGTTCATCC TAGCAAAAAT CTCACCATCT TCTATCAC

48

(2) INFORMATION FOR SEQ ID :1186:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1186:

30

ACATCATCCG AGTCCCCTCT ACAGTGTTC TGTGATCGT TGCATCCCCC

50

TGGTTTGAA ATAAAATATA AACTGCCCCG CAAGAGATAA AATTGTATTT

100

TTTA

104

35

(2) INFORMATION FOR SEQ ID :1187:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

602

(xi) SEQUENCE DESCRIPTION: SEQ ID :1187:

CTGGTTCTGT TTCTCGCAGG TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG 50
5 AGAATCCTAT TCAGTGCTCC CTTAGA 76

(2) INFORMATION FOR SEQ ID :1188:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1188:

20 AATAGGGCGC GATCAACTCT TAACTTTGAG GAGAACCAAC AA 42

(2) INFORMATION FOR SEQ ID :1189:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1189:

GGCGGACGTG CGCGCCTTGT CTTGCGGCA CCTGGGCCTG AGGTGCGTGC 50
35 CTCCCGGGCC CTCGCCAGCT CCAGATGCGT GAGGAGGACT TCAGAAACCC 100
GACTGAGAAG TGGAGCAACC CCCAGGAAGG GCCGGACCTG CCTAAATGCC 150
40 GCCAAGGCCT TTTATTTATG GCTAGTTTGC TCTCGTGAAA TACTAACATC 200
GTTTAAATGG CACTCATCAA GTACGCAAAT GATATGATTT AACCTCGCGC 250

603

AAT

253

(2) INFORMATION FOR SEQ ID :1190:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1190:

15 GAGGATCCAC CAACCATAGA ACGGCCCTAC TAATGAACCA CACAAGCTAG 50
TTGCACCACT ATAGAAACAC AAAACTACAC ATCTATACCA ATAAAAATAA 100
CAACTACTCC AATTGCCCAT GTGGTATTGT CGCAGACTGA AATGAATTAT 150
20 GAATTAGGT TGGTTACCAA TATCGGCATA AAATAAACTR TGTAAGGCTC 200
AMTATGTTGA CAGTAAGCTC TTGTCAGGTG TCTAATGAGG TAAAAGCATT 250
25 TT 252

(2) INFORMATION FOR SEQ ID :1191:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1191:

40 GAGGATCCAA CAACCATAGA GCACATAAAA ACCGCCCAAC GATCTAACTA 50
ATATACAACG GCTAACCGGG CCATTCAAAA GCTCGCCCAG ATTAAATGCC 100

604

TGCCGANAGC AAGTACATGG GGAGGATTAC TACTTCCTGG TTGCCAACCA 150
CCCTTCCGGC TGCCCTTGTG TTGACTTG 178

5 (2) INFORMATION FOR SEQ ID :1192:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1192:

GGATCGGCGG TAATCGGTGA GCTCGGTGTC GGGTAAGGGA CCCAGTCCAT 50
CGCCACCAAG CGCCAGGAAT GGGCAGCATA AGGGAAGGCT AAGGAGGACT 100
20 GCAACAGGTT AGGGCCCTGG AGATTGTATT TAGCAAGGGT ACCTGCGNNG 150
NGGGCA 156

25 (2) INFORMATION FOR SEQ ID :1193:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1193:

ATTCTGAATC TTTAATGAAA ATCAGCCCAG AGCTTGTTGT AATACAGACA 50
TAACTGCAAG AGCATGCCCA CAGCTTAGAG AGGTTGTACC AAATTTAGA 99

40

605

(2) INFORMATION FOR SEQ ID NO: 1194

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1194:

NNNNTCCTTC TCCTGCGACA GACA

24

15

(2) INFORMATION FOR SEQ ID NO: 1195

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1195:

TGTCTGTCGC AGGAGAAGGA

20

30

(2) INFORMATION FOR SEQ ID NO: 1196

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1196:

AANNTCTCGG ACAGTGCTCC GAGAAC

26

606

(2) INFORMATION FOR SEQ ID NO: 1197

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1197:

TTNNTCTCGG ACAGTGCTCC GAGAAC

26

15

(2) INFORMATION FOR SEQ ID NO: 1198

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1198:

GTTCTCGGAG CACTGTCCGA GA

22

30

(2) INFORMATION FOR SEQ ID NO: 1199

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1199:

GTTCTCGGAG CACTGTCCGA GAG

23

607

(2) INFORMATION FOR SEQ ID NO: 1200

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1200:

GTTCTCGGAG CACTGTCCGA GAC

23

15

(2) INFORMATION FOR SEQ ID NO: 1201

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1201:

CTGTCTGTCG CAGGAGAAGG AA

22

30

(2) INFORMATION FOR SEQ ID NO: 1202

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1202:

CTGTCTGTCG CAGGAGAAGG AG

22

608

(2) INFORMATION FOR SEQ ID NO: 1203

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1203:

AGCTCGGCTC GAGTCTG

17

15

(2) INFORMATION FOR SEQ ID NO: 1204

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1204:

GCGACAGACA GCAGACTCGA GCCG

24

30

(2) INFORMATION FOR SEQ ID NO: 1205

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1205:

GATCCGGCTC GAGT

14

609

(2) INFORMATION FOR SEQ ID NO: 1206

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1206:

CCGAGAACAC TCGAGCCG

18

15

(2) INFORMATION FOR SEQ ID NO: 1207

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1207:

GTAAAACGAC GGCCAGT

17

30

(2) INFORMATION FOR SEQ ID NO: 1208

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1208:

CGAGGTCGAC GGTATCG

17

610

(2) INFORMATION FOR SEQ ID NO: 1209

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1209:

CGAGGTCGAC GGTATCG

17

15

(2) INFORMATION FOR SEQ ID NO: 1210

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1210:

TACGTTCGAC AAGCTTGAAT TCGCGGCCGC TTTTTTTTTT TTTTTTTTTT

50

TTTTTT

56

30

(2) INFORMATION FOR SEQ ID NO: 1211

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1211:

611

11

GCCWSCGCCG A

(2) INFORMATION FOR SEQ ID NO: 1212

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1212:

GGTGGCGACG ACTCCTGGAG CCCG

(2) INFORMATION FOR SEQ ID NO: 1213

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1213:

TTGACACCAG ACCAACTGGT AATG

In the above SEQUENCE LISTINGS, some sequences are preferred because they fall into the category of sequences referred to hereinbefore which exhibit no more than 90% homology to a human sequence known per se. The preferred sequences in these terms are all of sequences SEQ ID Nos 1 to 1193, EXCEPT FOR SEQ ID Nos:

85, 117, 177, 197, 223, 248, 317, 354, 355, 483, 829, 1057, 594, 595, 597, 164, 427, 420, 58, 67, 374, 373, 501, 569, 188, 550, 904, 932, 97, 89, 134, 433, 434, 357, 4, 6, 11, 336, 529, 544, 545, 549, 1037, 847,

612

870, 871, 872, 873, 875, 876, 579, 199, 524, 544, 513, 380, 276, 291,
615, 623, 627, 634, 635, 648, 652, 617, 619, 684, 697, 718, 720, 1127,
1145, 1148, 1164, 938, 587, 589, 588, 241, 243, 335, 61.

5

10

15

CLAIMS:

1. A nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-

5 (a) a sequence selected from SEQ ID Nos 1 to 1193;

(b) an allelic variation of a sequence as defined in (a); or

10 (c) a sequence complementary to (a) or (b).

2. A nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof.

15 3. A sequence as claimed in claim 2 and which exhibits no more than 90% homology to a human sequence known per se.

20 4. A nucleic acid fragment comprising a portion of a sequence as defined in claim 2 or claim 3 of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridize to said sequence as defined in claim 2 or claim 3.

5. A fragment as claimed in claim 4, wherein said portion is at least 15 bases in length.

25 6. A fragment as claimed in any one of claims 1, 4 or 5 and encoding at least a portion of a biologically active polypeptide.

30 7. A nucleic acid sequence as claimed in claim 2 or claim 3 and encoding at least a portion of a biologically active polypeptide.

8. A DNA construct comprising a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7, together with a control or regulatory sequence.

35 9. A construct as claimed in claim 8 which encodes a fusion protein comprising a known protein and the polypeptide encoded by said fragment or sequence.

40 10. A construct as claimed in claim 9, wherein the fusion protein encoded is a cleavable fusion protein having an endopeptidase recognition site positioned between codons corresponding to said known

protein and said fragment or sequence.

11. The use of a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7 to produce a gene.
12. A DNA fragment comprising a gene obtainable by the use defined in claim 11.
13. An expression vector comprising a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, a DNA construct as defined in any one of claims 8 to 10, or a DNA fragment as claimed in claim 12, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory sequence.
14. A vector as claimed in claim 13, wherein said vector control or regulatory sequence comprises a regulatable promoter.
15. Host cells which incorporate as a heterologous part of their expressible genetic information a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, or a DNA fragment as defined in claim 12.
16. A process for the production of a polypeptide comprising cultivating host cells as defined in claim 15.
17. An antibody directed against a polypeptide obtainable by the performance of a process as defined in claim 16.
18. An antibody as claimed in claim 17 and which is monoclonal.
19. A novel gene product or portion thereof encoded by a fragment as defined in any one of claims 1, 3, 5 or 6, or encoded by a sequence as defined in any one of claims 2, 3 or 7, or encoded by the gene comprised in a DNA fragment as defined in claim 12.



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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification n 5 : C12N 15/11, 15/62 C12P 21/08, C07K 15/28 C12Q 1/68</p>	<p>A3</p>	<p>(11) International Publication Number: WO 94/01548 (43) International Publication Date: 20 January 1994 (20.01.94)</p>	
<p>(21) International Application Number: PCT/GB93/01467 (22) International Filing Date: 13 July 1993 (13.07.93) (30) Priority data: 13 July 1992 (13.07.92) GB-9214857.6 (71) Applicant (for all designated States except US): MEDICAL RESEARCH COUNCIL [GB/GB]; 20 Park Crescent, London W1N 4AL (GB). (72) Inventors; and (75) Inventors/Applicants (for US only): SIBSON, David, Ross [GB/GB]; 37 Grimsdells Lane, Amersham, Buckinghamshire HP6 6HF (GB). GROSS, Jacqueline [GB/GB]; 47 Boxmoor Road, Kenton, Middlesex HA3 8LH (GB). HADFIELD, Kathryn, Mary [GB/GB]; 5 Carlisle Terrace, St Ives, Huntingdon, Cambridgeshire PE17 4PQ (GB). HOWELLS, David [GB/GB]; 77 Puttocks Drive, Welham Green, Hatfield, Hertfordshire AL9 7LW (GB). STARKEY, Michael [GB/GB]; 27 Creasy Close, Abbots Langley, Hertfordshire WO5 0HS (GB). KELLY, Maria [IE/GB]; 24A Oxford Road, Ealing, London W5 3ST (GB). SHAW, Diana [GB/CA]; 342 Glacier Hall, University of Calgary, 2500 University Drive NW, Calgary, Alberta T2N 1N4 (CA).</p>		<p>(74) Agent: BIZLEY, Richard, Edward; Hepworth Lawrence Bryer & Bizley, 2nd Floor Gate House South, West Gate, Harlow, Essex CM20 1JN (GB). (81) Designated States: AT, AU, BB, BG, BR, BY, CA, CH, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 31 March 1994 (31.03.94)</p>	
<p>(54) Title: HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW</p>			
<p>(57) Abstract</p>			
<p>This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.</p>			

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CS	Czechoslovakia	MC	Monaco	TC	Togo
CZ	Czech Republic	MG	Madagascar	UA	Ukraine
DE	Germany	ML	Mali	US	United States of America
DK	Denmark	MN	Mongolia	UZ	Uzbekistan
ES	Spain			VN	Viet Nam
FI	Finland				

INTERNATIONAL SEARCH REPORT

International Application No

PCT/GB 93/01467

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all) ⁶			
According to International Patent Classification (IPC) or to both National Classification and IPC ⁷			
Int.C1.5	C 12 N 15/11	C 12 N 15/62	C 12 P 21/08
C 07 K 15/28	C 12 Q 1/68		

II. FIELDS SEARCHED	
Minimum Documentation Searched ⁷	
Classification System	Classification Symbols
Int.C1.5	C 12 N C 12 Q C 07 K

Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched ⁸
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III. DOCUMENTS CONSIDERED TO BE RELEVANT ⁹		
Category ¹⁰	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
Y	SCIENCE vol. 252, 21 June 1991, LANCASTER, PA US pages 1651 - 1656 ADAMS, M. ET AL. 'Complementary DNA sequencing: expressed sequence tags and human genome project' see the whole document	1-19
Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA vol. 88, March 1991, WASHINGTON US pages 1943 - 1947 PATANJALI, S. ET AL. 'Construction of a uniform-abundance (normalized) cDNA library' cited in the application see the whole document	1-19

<p>¹⁰ Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p>	<p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"G" document member of the same patent family</p>
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IV. CERTIFICATION	
Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report
08-10-1993	01.03.94
International Searching Authority	Signature of Authorized Officer
EUROPEAN PATENT OFFICE	ANDRES S.M.

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		Relevant to Claim No.
Category	Citation of Document, with indication, where appropriate, of the relevant passages	
Y	NUCLEIC ACIDS RESEARCH vol. 18, no. 19, 11 October 1990, ARLINGTON, VIRGINIA US pages 5705 - 5711 KO, M.S.H. 'An 'equalized cDNA library' by the reassociation of short double-stranded cDNAs' cited in the application see the whole document	1-19
Y	--- NATURE vol. 355, 13 February 1992, LONDON GB pages 632 - 634 ADAMS, M. ET AL. 'Sequence identification of 2,375 human brain genes' see the whole document	1-19
Y	--- GENE vol. 81, 1989, AMSTERDAM NL pages 295 - 306 AKOWITZ, A. & MANUELIDIS, L. 'A novel cDNA/PCR strategy for efficient cloning of small amounts of undefined RNA' see the whole document	1-19
P,Y	--- WO,A,9302214 (MEDICAL RESEARCH COUNCIL) 4 February 1993 see the whole document -----	1-19

INTERNATIONAL SEARCH REPORT

International application No
PCT/GB93/01467

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos. because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos. because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos. because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see PCT/ISA/206 mailed on 29.11.93

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-19(all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

**ANNEX TO THE INTERNATIONAL SEARCH REPORT
ON INTERNATIONAL PATENT APPLICATION NO.**

GB 9301467
SA 76316

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report.
The members are as contained in the European Patent Office EDP file on 02/02/94
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A- 9302214	04-02-93	None	

EPO FORM P0479

For more details about this annex : see Official Journal of the European Patent Office, No. 12/82